

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model.

Run on: January 21, 2006, 07:52:59 ; Search time 396 Seconds
(without alignments)
2797.533 Million cell updates/sec

Title: US-10-066-521-6
Perfect score: 7074
Sequence: 1 MEGAKSLTFSSYGLQMKLYE.....DDHSGVSWSLGAGLEGLVS 1344

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6049916 seqs, 412136615 residues
Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-Model=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.apoc/US1006521/runat_20012006_145900_21124/app_query.fasta.1.1543
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rmpbn -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US1006521_@CEN_1_1_277_@runat_20012006_145900_21124
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCOT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.1.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.2.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1248.5	17.6	3189	8 US-11-137-465-10	Sequence 9, Appl1
2	1217	17.2	3150	8 US-11-137-465-9	Sequence 10, Appl1
3	957	13.5	5100	8 US-11-136-527-4000	Sequence 4000, Ap
4	364	5.1	4390	8 US-11-136-527-4006	Sequence 4006, Ap
5	359.5	5.1	3382	7 US-10-966-846-1	Sequence 1, Appl1
6	347	4.9	2859	7 US-10-966-846-3	Sequence 3, Appl1
7	280	4.0	3213	8 US-11-147-047-23	Sequence 23, Appl1

8	276	3.9	3072	8 US-11-145-631-3	Sequence 3, Appl1
9	276	3.9	3133	8 US-11-136-527-4003	Sequence 4003, Ap
10	276	3.9	3133	8 US-11-145-631-1	Sequence 1, Appl1
11	276	3.9	3612	8 US-11-145-631-6	Sequence 6, Appl1
12	276	3.9	3615	8 US-11-145-631-4	Sequence 4, Appl1
13	276	3.9	3615	8 US-11-145-631-12	Sequence 12, Appl1
14	270	3.8	536	8 US-11-128-061-276	Sequence 276, App
15	270	3.8	536	8 US-11-128-061-3918	Sequence 3918, Ap
16	270	3.8	536	8 US-11-128-049-276	Sequence 276, App
17	270	3.8	536	8 US-11-128-049-3918	Sequence 3918, Ap
18	169.5	2.4	1068	7 US-10-750-185-27825	Sequence 27825, A
19	169.5	2.4	1068	7 US-10-750-623-27825	Sequence 27825, A
20	168.5	2.4	1215	8 US-11-147-047-22	Sequence 22, Appl1
21	166	2.3	1925	7 US-10-750-185-55918	Sequence 55918, A
22	166	2.3	1925	7 US-10-750-623-55918	Sequence 55918, A
23	151	2.1	1400	8 US-11-136-527-8099	Sequence 8099, Ap
24	149	2.1	2148	8 US-11-155-288-28	Sequence 28, Appl1
25	149	2.1	2148	8 US-11-155-288-28	Sequence 28, Appl1
26	146.5	2.1	2144	7 US-10-624-932-15	Sequence 15, Appl1
27	145.5	2.1	2187	7 US-10-624-932-17	Sequence 17, Appl1
28	143	2.0	6111	8 US-11-136-527-3837	Sequence 3837, Ap
29	143	2.0	5984	8 US-11-091-928-3	Sequence 3, Appl1
30	138.5	2.0	5366	8 US-11-136-527-4096	Sequence 4096, Ap
31	136.5	1.9	3573	8 US-10-632-150-53	Sequence 53, Appl1
32	135.5	1.9	1681	7 US-11-073-467-53	Sequence 53, Appl1
33	135.5	1.9	1681	8 US-11-073-467-53	Sequence 53, Appl1
34	135.5	1.9	1681	8 US-11-073-467-53	Sequence 53, Appl1
35	135.5	1.9	6269	8 US-11-136-527-2572	Sequence 3808, Ap
36	134	1.9	9136	8 US-11-136-527-2808	Sequence 47, Appl1
37	133.5	1.9	4059	7 US-10-632-150-47	Sequence 47, Appl1
38	133.5	1.9	4059	8 US-11-073-467-47	Sequence 47, Appl1
39	133.5	1.9	4059	8 US-11-073-467-47	Sequence 47, Appl1
40	132.5	1.9	1320	7 US-10-750-185-60781	Sequence 60781, A
41	132.5	1.9	1320	7 US-10-750-623-60781	Sequence 60781, A
42	132.5	1.9	7474	8 US-11-069-834-49	Sequence 49, Appl1
43	132	1.9	3103	7 US-10-821-234-224	Sequence 224, App
44	130.5	1.8	33018	8 US-11-077-716-1	Sequence 1, Appl1
45	129.5	1.8	116856	8 US-11-143-980-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-11-137-465-10
Sequence 10, Application US/11137465
Publication No. US2005025558A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Xiang, Zhaoqing
APPLICANT: Kahlack, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
CURRENT APPLICATION NUMBER: US/11/137,465
FILE REFERENCE: GPS0018
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/US01/09226
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 3189
TYPE: DNA
ORGANISM: Homo sapiens

US-11-137-465-10

Alignment Scores:

Pred. No.:	1.15e-105	Length:	3189
Score:	1248.50	Matches:	335
Percent Similarity:	47.17%	Conservative:	199
Best Local Similarity:	29.59%	Mismatches:	459
Query Match:	17.65%	Indels:	139
		Gaps:	23

US-10-066-521-6 (1-1344) x US-11-137-465-10 (1-3189)

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Qy 12 TyrlgyleuglntrpCyseuTyrcgluleuApylsglunghpnehlnthrPheylsglu 31
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Db 25 TTCAACTGCGAGGCTCTCTGAGCAGCTCAGCAGATGAGTGAAGCAATTGACAGAT 84
Qy 32 LeuleuYslylsrsergluserThrCyserllleProglPhegluilegu 51
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 85 CTGATCAAGACCTTCTCTGAGCAGAGCTCCAGAGATCCCCCAAGAGAGTGAAC 144
Qy 52 AsnlaAnValglucyVleuValleuLeuuhlsaglutyryrglyAlaserleuAla 71
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 145 AAGCGTAGTGGAGCACTGTGAAATCTTCAACCCATGTGTACAGCTACTGGGTG 204
Qy 72 TrpalatHserllserlllePhegluAmetAseuAgtHrleuSergluylsAla 91
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Db 205 GAGATGGCGAGCTCCAGGCTTTGAAAGATGACCGAATGATCTGTGTGAGAGCA 264
Qy 92 ArgAhpMetlylsylserglAlaMetglunglu----- 105
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 265 AAGGATGAAGTCAGAGAGCAGCTTGTGAATCTTTAATAAGAGAGCTTATCATTA 324
Qy 106 GlYAlatHrAlaIagluThrgluInglunlIlelelglAlaMetglungluYl 125
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Db 325 GGGATACACGGAAGAACCAACCTCTAGCGTGAAGATGCTGAGCGCTTCAA 384
Qy 126 AlatHrAla--AlagluThrgluInglunlYhis-----GlyglYAspThr 140
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 385 ACAGACGACAGAGGTTTACAGAAACAGAAAGAAATCATCTGCTGGTAAAGAGTC 444
Qy 141 TrpAhpTyrlYsSerHis-----ValMetHrlyAspPhe 151
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Qy 152 AlagluIngluAerValArgArgserPhegluAanthrAlaIaAspTrpProgluMet 171
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Db 505 -----CGGAGATGTGAGAGAGCTGGCTTGAGATGAGAAAGAGTCC 546
Qy 172 GlntHrleuAlaglyAlaPheAspSerAhpArgTrpIlyPheArgProArg----- 188
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 547 CAGGTTATGGCTGAGATCAAGATGCTGATCCCATTCAGAACCCAGAGGTGCTTCCC 606
Qy 189 -----ThrValleuuhlsaglutyrylserglYlleglYlsSerAlaLeu 203
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Db 607 GGGGCTTTCATACACGGTGTGTCTGTATGTCTCTGAGGCTTGGGAAAACACAGGTG 666
Qy 204 AlAhpArgTlleValleuCystrpAlaglnlYglYleuTyrglnlYmetPheSerTy 223
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 667 GCCCAAGAACTAATGCTAGCTAGGAGGAGCAACCTCATTCAC--AAATTCAAATAT 723
Qy 224 ValPhePheleuProValArgIumecInArglylsrsergluserSerValThrgluPhe 243
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Db 724 GCGTTTACCTCAGCTGAGGAGACTCAGCCGCTGGGCCCGTGCAGATTGGCAGAGTGT 783
Qy 244 lIleSerArgIutrpProAspSerGlAlaProValThrgluIlleMetSerArgProglu 263
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 784 GTCTTACAGGAGCTGCTGATGATGACAGATGACATTCACATCTCTAGCCCAAGACAG 843
Qy 264 ArgleuLeuPheIlelleAspGlyPheAspIleuYlser-----ValleuAasn 280
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 844 AAAATCTTGTCTGTATGAGCGCTTGTATGAGCTGGAGCGGACCTGGGGCGCTGATC 903
Qy 281 AsnAhpThrlylsleuCyVleuAspTrpAlagluYlsInpProPheThrlleuIleArg 300

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Db 904 GAGAGC-----ATCTCGGGAGCTGGAGAGAAAGACCGGTGCGCTCTCTGGGG 957
Qy 301 SerleuLeuArglylsValleuLeuProgluserPheleuIleValThrValArgAerVal 320
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 958 AGTTGTGAACAGGAGTGAATTTACAAAGCGCCCTGTGTGTGACACAGCGGCCCAAG 1017
Qy 321 GlYThrgluYlsleuYlsSergluValIleSerProArgTyrlYleuLeuValArgglYlle 340
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1018 GCGCTTAGAGAGACTCCGAGTCTGCGGAGAGAGCCATCTACATTAAGGTGAGAGGCTTC 1077
Qy 341 SerglYglunlArgllleHlsleuLeuInglunlYlleglYlunHlsInlYleThr 360
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1078 CTGAGAGAGAGACAGAGAGGCTATTCTTGACACATTTGGAGACAGACCAAGCATG 1137
Qy 361 GlnglYleuArgAlaIleMetAasnAhpArgIleuLeuAerIncyVglInValProAla 380
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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Qy 381 ValglYserleuIleCyValAlaleuGlInleuGlInAerValValglYluserValAla 400
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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Qy 401 ProPheAasnGlntHrleuThrglyleuuhlsAlaAlaPheValPheHlsGlInleuThrPro 420
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Db 1258 CCCACCTGCTCCACCCGACGAGGAGTGTCTGCTGCTCTGTCAGCCGAGTTC---CCG 1314
Qy 421 ArgglYValValArgArgCyVleuAasnleuGlunlYglValleuYlsArgPheCyV 440
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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Qy 441 ArgMetAlaValglunlYValTrpAasnArglylsSerValPheAerglYAspAerleuMet 460
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1354 CTCTGGGCCCGGACAGGCGCTGTGGGCCGACAGCTCCGTCTTACCGAGAGAGATCGGA 1413
Qy 461 ValglnlYleuArglylsSergluYleuAglAlaLeuPheHlsMetAanlleuLeuPro 480
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1414 AGGCTCGGGGTGAGAGAGTCCGACCTCGTGTCTCTGACGAGACATCTCCGCGAG 1473
Qy 481 AspSerHlsCyseuInglutyrylThrThrPhePheHlsleuSerleuGlInAerPheCyAla 500
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1474 GACAGAGTCTCCAAAGGCTGTACTCTTATCCACTCCAGCTTCCAGAGTTTCTACT 1533
Qy 501 AlaleuTyryValleuInglunlYleuGlun----- 510
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1534 GCGCTGTCTTACACCTCGGAGAGAGAGAGAGATAGAGAGCGGACACCTGGAGAC 1593
Qy 511 -----lIlegluProAlaleuCyVProleuTyryValglunYthrlYlsArgSerMet 527
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1594 ATTGGGAGCTACAGAGAGCTGTCTTCCGGA-----GTAGAAAGATCC--AGGAGCCCC 1644
Qy 528 GluleuYlsInlAglyPheHlsIleHlsSerleuTrpMetlylsArgPheleuPheglY 547
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1645 GACCTGTATCCAAAGAGGCTAC-----TACTCTTTGGC 1677
Qy 548 LeuValSergluAerValArgArgProleuGlunValleuIngluCyVProValProleu 567
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1678 CTGCGTACAGAGAGAGAGAGAGAGATGAGAGGCTTTGGCTGCCGATGTCAACG 1737
Qy 568 GlYVallylsIngluYlsleuLeuuhlsTrp--ValSerleuInglunlInpProAanAla 586
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1738 GACATCAACAGGAATGTGTGATGAGATGATGATGATGATGATGATGATGATGATGATG 1797
Qy 587 ThrThrProglAerThrlleuAerAlaPheHlsleuYlsleuPheglunlYlsInlYglu 606
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1798 ACA-----GACCTGACAGAGCTCTCGGCTGTGTGACAGTCTGAGAGAGAGAG 1848
Qy 607 PheValArgleuAlaleuAasnserPheglunlValTrpIleuProIleAasnleu 626
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1849 CTGCTGAAGAGAGTGTGAGCTCACTTCAAAATAATCCCTGACCTTAATGCA--GTA 1905
Qy 627 AspIleuIleAserSerPheCyVleuInlHlsCyVProTyrlYleuAglYlsIleArgVal 646
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db 1906 GACGTGTGACCATCTTCATCTGCGTCAGAACGATGCGAACCCTGACGAAATATGCTACTG 1965
Qy AspVal---LysGlyIlePheProArgAspGlnSerAlaGluAlaCysProValPro 665
Db 1966 CAGGTAATTAAGAGAAATCTCCGAGAAATGTCACCTGCGTGAATTCAGACCGCAGGTT 2025
Qy LeuTrpMetCysAspArgLysThrLeuIleGluGlnIleProGluAspPheCysSerMetLeu 685
Db 2026 GAGAGATCCCAAGATGATCAGACACATGCTTCCTTCTGAGAGACCTTGTTCATATTT 2085
Qy 686 G1YThriHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAla 705
Db 2086 GGATCAAAATTAAGATCTGATGGGTCTAGCAATCAATGATAGCTTTCTGAGCTCCCTTA 2145
Qy 706 MetLysThrLeuCysAlaLeuLeuArgHisProThrCysLysIleGlnThrLeuMetPhe 725
Db 2146 GTAAGATCTCTGTGAGCAAAATACCTCTGACACCTGTCACTGACAGAGATGATGTC 2205
Qy 726 ArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArg 745
Db 2206 AAAAACAATTTCCCAAGCTGATGCTCATGGAACCTTCTGACCTTCAGAGTCAACAG 2265
Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThriHisLeuLysGluGluAspValArgMetAla 765
Db 2266 ACTGTAAGTATCTGACCTTCAGAGCAAT-----GACAGAGATATGATTTCCCGCA 2319
Qy 766 ---CysGluAlaLeuLysHisProLysCysLeuLeuGlnSerLeuArgLeuAspCys 784
Db 2320 TTGGTGTAGGCTTGTGAGCATCTCAGAAATGTAACCTGCAATCTCGGGTGTGTCTTGT 2379
Qy 785 GlyLeuThrHisValaCysLeuLysLeuLysIleSerGlnIleLeuThrThrSerProSerLeu 804
Db 2380 TCCGCTACCTACGACGAGTGGCTGATCTCTCTTGGCCCTTGAAGTCAACAGCTCCCTG 2439
Qy 805 LysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAsp 824
Db 2440 ACGGCGTAACCTTCGCAAGATAGCTTCGATGAGGGGTGAAGTGTCTGATACACA 2499
Qy 825 AlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThr 844
Db 2500 ACTTGTAGACACCCCAAGTGTCTTGTGCAAGGTTGTGCTGGAACCTGTCACCTTCA 2559
Qy 845 AlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeu 864
Db 2560 GAAGCAATTTGCAAGACCTTGTCTGTGTGTTGTCAGCCGGAAGTCAACACCTG 2619
Qy 865 CysLeuSerAsnAsnSerLeuGlyValGlnGlyValAsnLeuLeuCysArgSerMetArg 884
Db 2620 TGCCTTGGCCAGAAACCCCATTTGGAAATACAGGGGTGAAGTTTCTGTGTAGGGCTTGAAG 2679
Qy 885 LeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGly 904
Db 2680 TACCCCGAGTGAACCTGACAGACCTTGGTGTGGAACCTGCAATGACATGACATGACATG 2739
Qy 905 CysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSer 924
Db 2740 TGCCTCGATCTTCACAAACCTTTCACAGAAAATATAGCCCTGTGTGTGATTTGGAGG 2799
Qy 925 MetAsnProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgGluProSer 944
Db 2800 CTGAATCACAATGAGATTAAGGAGATGAAGTTCCCTGTGTAGAGGCTTTGAGGAACCACTG 2859
Qy 945 CysHisLeuGlnAspLeuLeuValLysCysHisLeuThrAlaAlaCysCysGluSer 964
Db 2860 TGCACACTTG-----AGATGT----- 2874
Qy 965 LeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAla 984
Db 2874 ----- 2874
Qy 985 LeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeu 1004
Db 2874 ----- 2874

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Qy 1005 ThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeu 1024
Db 2875 -----CTGTGGTGTGGGAGATGTTCCATCCCTCGTCAAGTTGAAAGACTGTGCTCT 2928
Qy 1025 AlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAspSerPro 1044
Db 2929 GCCCTCAGCTCAACAGAGCTCTGTGACCTGTGACCTGGGTGAGAAATCCCTTGGGCTCT 2988
Qy 1045 LysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIle 1064
Db 2989 AGTGAGAGAAAGATGCTGTGAAAACCTTGACATGTTCCAGTGGACACCTCGGAGACTC 3048
Qy 1065 GlyLeuTrpLysTrpGlnTrpProValGlnIleArgLysLeuLeuGluGluValGlnLeu 1084
Db 3049 AGGTGAAATACGATGACTTAAATGATGACATCAATAGCTGCTGGAAGAAATAGAAAGA 3108
Qy 1085 LeuLysProArgValAlaIleAspGlySerTrpHis 1096
Db 3109 AAAAACCAACATGATATGATATGATGAGAAACAT 3144

RESULT 2
US-11-137-465-9
; Sequence 9, Application US/11137465
; Publication No. US2005025558B1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPE50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-137-465-9

Alignment Scores:
Pred. No.: 1,01e-102 Length: 3150
Score: 1217.00 Matches: 333
Percent Similarity: 47.88% Conservative: 187
Best Local Similarity: 30.66% Mismatches: 470
Query Match: 17.20% Indels: 96
DB: 8 Gaps: 22

US-10-066-521-6 (1-1344) x US-11-137-465-9 (1-3150)
Qy 8 ThrPheSerSerTyrgLysLeuGlnTrpCysLeuTy-----GluLeuAspLys 23
Db 76 ACTATGACATCGCCCAAGCTAGAGTGAAGTCTGACAGACCTTTCGACAGCAGCTGAACGAG 135
Qy 24 GluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerSerThrThrCys 43
Db 136 GATGATTAAGAGATTTAAATCCCTTTATGAGGCTTTTCCCTGGAAGAGCTGTACAG 195
Qy 44 SerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHis 63

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Db 196 AAGACCCATGCTGATGAGTGAAGAGCTGATGCAAGAACTGGCAGAAATTCCTGTC 255
Qy 64 GlnTyrTyrGlyAlaSerLeuAlaTPrAlaThrSerLeuSerLeuPheGluAenMetAen 83
Db 256 AAGACCTCTCCAGAAAATTTGATTAAGGAATGCCACTGTGAACACTTTGGAAAGATTAAT 315
Qy 84 LeuArgThrLeuSerGlnTyrAlaArgAspMetLeuTyrValSerGlnAlaMetGlu 103
Db 316 CTCACGGAAATTTGTAAAGATGCGAAAGCTGAGATGATGAGACGGAACGGCTGCAAGA 375
Qy 104 GlnGlnGlyAlaThrAlaAlaGluThrGlnGlu--GlnGluLeuSerGlnAlaMetGlu 122
Db 376 ATGATTAATCTGAGCTGGAGATGACAGAAAGACTCGGAGTTAAGCAAGACGAGTGA 435
Qy 123 GlnGlnGly--AlaThrAlaAlaGluThrGlnGlnGlnGlnGlnGlnGlnGlnGln 141
Db 436 AAGGAAAGATGAGAAATTCATATGAGAAACAGCTTTGGTCTGGAAGAACCTTTTGG 495
Qy 142 AspTyrTyrSerHisValMetThrLeuPheAlaGluGluAerValAlaArgSer-- 160
Db 496 CAAGGAGAC-----ATTGACAAATTCATATGACAGCTCACTGAGAAACCAACGG 546
Qy 161 -----PheGluAenThrAlaAlaAspTyrProGlnMetGlnThrLeuAlaGlyAla 177
Db 547 TTCATTCATTTCTTGAATCCAGAAC-----CCAGAAAGCTAAC----- 588
Qy 178 PheAspSerAspArgTyrGlyPheArgProArgThrValValLeuHisGlyLeuSerGly 197
Db 589 -----CCTTACACGGTGTGTGCTGACGGCCCGCCGAGGC 621
Qy 198 IleGlyLeuSerAlaLeuAlaArgArgIleValLeuGluTyrTrpAlaGlnGlyLeuTyr 217
Db 622 GTGGGAAACACACGCTGGCCAAAAGTGAATGCTGACAGCTGACAGACTGCAACTC--- 678
Qy 218 GlnGlyMetPheSerTyrValPhePheLeuProValAlaArgGlnMetGlnArgGlyLeu 237
Db 679 AGCCCGACGCTCAGATACGGCTTCTACCTCAGCTGACAGAGAGCTCAGCCGATGGCCCC 738
Qy 238 SerSerValThrGluPheIleSerArgGluTyrProAspSerGlnAlaProValThrGlu 257
Db 739 TGCGATTTGCAGAGCTGATCTCCAAAGACTGCGCTTAATTTGACGATGACATTTCAAGC 798
Qy 258 IleMetSerArgProGlnArgLeuLeuPheIleLeuArgPheAspMetLeu----- 275
Db 799 ATCTTAAGCCCAAGACAGAGAAATCTGTTCGTGTCATGAGCTTGAAGCTGAAAGTC 858
Qy 276 -----GlySerValLeuAsnAspThrLeuLeuGlnGlnGlnGlnGlnGlnGln 293
Db 859 CCACCTGGGGGCTGATCCAGAC-----ATCTGGGGGACTGGGAGAGAGAGAG 909
Qy 294 ProProPheThrLeuIleArgSerLeuLeuArgGlyValLeuLeuProGlnSerPheLeu 313
Db 910 CCGGTGCCCCCTCTCTGGGAGTTTGTCTGAAGAGAAAGATTTACCAAGGCGCCCTTG 969
Qy 314 IleValThrValArgAspValGlyThrGluLeuLeuSerSerGlnValAlaSerProArg 333
Db 970 CTGGATCCACACGCGGCCCAAGGCACTGAGGAGACTTCAAGCTCTGGGCGCAGACCAATC 1029
Qy 334 TyrLeuLeuValArgGlyIleSerGlyLeuGlnArgIleHisLeuLeuLeuArgGly 353
Db 1030 TAGCTTAAGGCTGAGGGCTTCTGAGAGAGACAGAGAGGCGCTATTTCTTGACACTTT 1089
Qy 354 IleGlyLeuHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 373
Db 1090 GGAAGACAGAGACAGGCAATCGCTTGTAGCTTAAGAGAGCAACGCGCCCTGTTC 1149
Qy 374 AspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAsp 393
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Qy 394 ValValGlyLeuSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPhe 413

Db 1210 GAGAAAGGAGAGACCCGGTCCCACTGCTCAACCCGACGAGGCTGTTCCTGCTTC 1269
Qy 414 ValPheHisGlnLeuThrProArgGlyValAlaArgArgCysLeuAsnGlnGluArg 433
Db 1270 CTCTGACGCGGCTTC---CCGACAGGCGCA-----CAGCTGCGG 1305
Qy 434 ValValLeuLeuArgPheCysArgMetAlaValGlnGlyValIleThrAsnArgLeuSerVal 453
Db 1306 GCGCGCTGGGACGCTGAGCTCTGCGCGCCGACAGGCGCTGTGGCGCGAGATGCTCGTG 1365
Qy 454 PheAspGlyAspArgLeuMetValGlnGlyLeuGlyGlnSerGlnLeuArgAlaLeuPhe 473
Db 1366 TTCACCGAAGACCTTGAAAGCTTCGAGAGCTTCGAGAGTCCGACCTCGCTGTTCCTG 1425
Qy 474 HisMetAsnIleLeuLeuProAspSerHisCysGlnGluTyrTyrThrPheHisLeu 493
Db 1426 GAGGAGACATCTTCGCGCCAGACAGAGTCCAAAGCGCTGATCTTCAATCCACTC 1485
Qy 494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGlu----- 507
Db 1486 AGCTTCAGAGATTTCTCACTGCGCTGTCTACGCTCGAGGAGAGAGAGAGGAGGAGAC 1545
Qy 508 -----GlyLeuGlnIleGluProAlaLeuCysProLeuTyrValGlnGlyThr 523
Db 1546 AGGAGCGGCAACGCTGGACATCGGAGAGCTACAGAGCTGCTTCCGAGAAAGAGA 1605
Qy 524 LeuArgSerMetGlnLeuGlyGlnAlaGlyPheHisIleHisSerLeuThrMetLeuArg 543
Db 1606 CTCAGAAACCCGACCTGATTCAGATGA-----CAC 1638
Qy 544 PheLeuPheGlyLeuValSerGluAspValAlaArgArgProLeuGlnValLeuLeuGlyCys 563
Db 1639 TTTCTATTGCGCTCGCTTAAG 1698
Qy 564 ProValProLeuGlyValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 582
Db 1699 CGGATTCACCGGACAGCAACAAAGAAATTTCTCATGATGCAAGACATCTTCAACAAAT 1758
Qy 583 GlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThr 602
Db 1759 AAGCCTTATCCCTGAC-----GACCTGAAGAGAGTCTTGGGCTCCGTATGAGCTCT 1812
Qy 603 GlnAspGlyGlnPheValAlaGlyLeuAlaLeuAsnSerPheGlnGlnValIleProIle 622
Db 1813 CAGGAGGAGAGCTGGGAGAGAGTGTGTGCGCCCTGCAAGAAATTTCTAATCACTG 1872
Qy 623 AsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArg 642
Db 1873 ACAAAATCTTCTGAAGATGATGATTTGTTCTTCAAGCTGAAAGCATTTGTCAAGACTGAG 1932
Qy 643 LeuIleArgValAspVal---LysGlyIlePheProArgAspGlnSerAlaGluAlaCys 661
Db 1933 AAATCTTCATGCAAGTGAAGAGAGAGGAGGCTTC----- 1965
Qy 662 ProValProLeuThrMetArgAspLeuThrLeuIleGlnGlnGlnGlnGlnGlnGln 681
Db 1966 -----CTGAGAAATTAATAGATTTT 1986
Qy 682 -----CysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
Db 1987 GAATGAGACATTAATTTGAAGCTCAAAACAGAACTCAAGTTTCTGGAAGTAAACAA 2046
Qy 699 SerIleLeuThrGlnArgAlaMetLeuThrLeuGlyAlaValLeuAspArgHisProThrCys 718
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Qy 719 LysIleGlnThrLeuMetPheArgAspAlaGlnIleThrProGlyValGlnHisLeuTyr 738
Db 2107 CATCTGAGAAAGAGGATTAATAAACGTAACCCCTGACACCGGAGTCCGGACTTCTGT 2166
Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyThrHisLeuLeu 758
Db 2167 CTTCCTTCAATTTGGAAGAGACCTTCAAGCACTGACCTTGGAGGG---CAATCGAG 2223

Qy	759	Gluc1u1n6p-----ValAGMeAlaCyeglu1alaLeu1ySh1sProLyCyLeu1eu	776
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Qy	777	Glus1er1eulAryLeuAerCyCyeg1yLeuThrh1valaCyvTy1LeuLyv1sEser1n	796
Db	2284	CAGTAACTGAGGTTGGAGAGTCACTGTGTCCACCCCGAGCAGTGGGCTGAAATCTTCTAT	2343
Qy	797	1Le1euThrh1SerProSer1eul1ySer1eulSer1eulAgl1Agn1yVal1ThrAer	816
Db	2344	GTCTCTCAAGCCAAACCAAGTCCCTTAAGACCTGGCGTCTTACGCCAAATGCTCTGGAT	2403
Qy	817	Gln1yValMeTProLeuSerAAspAlaLeu1aryalSer1nCyvalA1eulG1n1yLeu	836
Db	2404	GAGGTGCGCATTTGTCTGTACAAACATGACACGCCCAAAACATTCCTGTCAATGTG	2463
Qy	837	1Le1euG1n1uAerCyvgl1y1eThralaThrs1yCyvG1nSer1eulA1sEralA1eulA	856
Db	2464	TCTGTGAAACTGTGCTGCTTACAGAAAGCCAGTTGCAAGACCTTGCTGTCTGTGGT	2523
Qy	857	Ser1nA1rgsSer1eulThrh1s1eulCy1eulSer1nA1nA1nSer1eulG1yA1nG1u1yAl	876
Db	2524	GTCCAGCAAGAGCTGACACACTGTGTGCTTCCAGAAACCCCATTTGGGGAATACAGGGGTG	2583
Qy	877	Aen1eul1euCyvA1rgsSerMeTArg1eupProH1sCyS1er1eulG1nA1rg1eulMe1uA1n	896
Db	2584	AAGTTTCTGTGTGAGGCGTTAGATTACCTGTATTTAACTGCAGACCTTGGTGTGGTG	2643
Qy	897	GlnCyvH1s1eulAerThrh1Agl1Cyvgl1yPhe1eulA1eulA1A1eulMeT1yA1nSer	916
Db	2644	TCTTGTTCGGCTACCACTCAGACAGGGGTGATGCTTCTCTTGGCCCTTGAAGTCAACAG	2703
Qy	917	Thr1eulThrh1s1eulSer1eulSerMeT1nProValG1nA1nA1nG1yVal1y1eul1eu	936
Db	2704	TCCCTGAGTGCAGTAACTCTGCCAACAATAGCTTGTGAATGAGGGTCTTAAGTTGCTG	2763
Qy	937	Cyeg1uValMeTArg1uProSerCyvH1s1eulG1nAer1eulG1u1eulVal1y1eCyvH1s	956
Db	2764	TACACAACTTGCAGACACCCCAAGTCTTTCTGCAGAGTGTGTCTTGAAAACGTGTAC	2823
Qy	957	LeuThralA1a1aCyCyvEgl1Ser1eulSerCyvA11sEserA1rgsE1rgh1b1eul1y	976
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Qy	977	Ser1eulAer1eulThrhA1nA1A1eulG1yA1nG1yVal1A1A1A1A1eulCyvEgl1y	996
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Qy	997	Leu1yEgl1yA1nSerVal1eulThrh1rgr1eulG1yLeu1yvalaCyeg1yLeuThrhSer	1016
Db	2944	TTGAGAGTACCCCGAGTGTAACTGACAGACCTTGTGTGTAA1CAAGCATGACAGATTAACAA	3003
Qy	1017	AerCyvCyvG1u1A1A1eulSer1eulA1A1eulSerCyvA1nA1nG1n1eulTh1Ser1eulA1n	1036
Db	3004	CTTGGCTGTAAATATCTCTCAGAGGCGCTCCAAAGAGCTGACGCTTCAAAACCTGTGAC	3063
Qy	1037	LeuValG1nA1nA1nA1nPheserProLyvEgl1yMeT1y1eulCyvSerA1A1Pha1aCy	1056
Db	3064	TTGAGATTAACAACAGATAGCT---CGTGAATTTGGAATTTCTGTCAAGCATTTAGAAAT	3122
Qy	1057	ProThrSerAen1eulG1n 1062	
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RESULT 3			
US-11-136-527-4000			
; Sequence 4000, Application US/11136527			
; Publication No. US20050287570A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William M			
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes			

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FILE REFERENCE: 031896-041000 (AM10101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ. ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4000
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: LENGTH: 5100
:
: TYPE: DNA
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: ORGANISM: Rattus norvegicus
US-11-136-527-4000

Alignment Scores:
Sred. No.: 5.12e-78
Score: 957.00
Percent Similarity: 36.13%
Best local Similarity: 23.83%
Query Match: 13.53%

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Db 232 CAGCTTCTGCTGCGCAATTAAAGCGACCTCCAGAGAGCTTCTGGGTGAGACACCGCTCAG 231
QY 49 GlnIleGlnAsnAlaAsnValGluCysPheuAlaLeuLeuLeuHISGluTyrTyrGlyAla 68
Db 292 CCGAGAGAAACAGATGGCATGGAGAGTGGCTGTAACCTGGTGGGTGAC---TATGGGAG 348
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGlnAsnMetAsnLeuAlaTyrThrLeuSer 88
Db 349 CAGGGGGCTGGGACCTAGCCTCATATCCTGGAGGACGATGGGCTGAGGCTACTGTGC 408
QY 89 GlnLysAlaIaArgPhe----- 93
Db 409 GCCCAAGCCAGGAAGGGGAGGCCACCTCTCCCTCATTCCTCAGAGCCAAAGTAAACC 468
QY 93 ----- 93
Db 469 CACCTGGGCTCTCCAGCCAAACCACTTCCACCGCAGTGTAAATGCCCTGGATCATGAA 528
QY 94 -----AspMetLysLysSerGlnAlaMetGluGln 104
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QY 105 GlnGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMet----- 121
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QY 121 ----- 121
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QY 122 -----GluGlnGluGly----- 125
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QY 125 ----- 125
Db 769 ACCCAATGGCTCTGATGATGAACGTCAAGAAATTACTACACAGAAATCAGAGAAAGAG 828
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Db 829 AGAGAGAAATCAGAGAAAGCAGAGCCGCCATGGGACGCGGTGAGAAACGCCCCACAG 888
QY 135 GlnHISGlyGly----- 138

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 Qy 233 GlnArgLysLysGlySerSerValThrGlnPheIleSerArgGluTrpProAspSerGln 252
 Db 1276 GCCCAGTCCAGAGTGGAGTCTGTGCTGAGCTCATCGAAAAGATGGGACAGCCACTCG 1335
 Qy 253 AlaProValThrGluIleMetSerArgProGlnArgLeuPheIleIleAspGlyPhe 272
 Db 1336 GCTCCCATAGACAGATCTGTCTAGCCCAAGAGCGGCTGCTTCATCTCGATGGTGTGA 1395
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 Db 1396 GATGAGCCAGATAGGTGCTTGCAGAGCCAGATTCAGCTGTGTGCAGCTGAGACAG 1455
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 Db 1456 CCACAGCCGGCGAGTGCATGCTGGGCAATTTGCTGGGAAACTATATCTCCGAGGCA 1515
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 Db 1516 TCCTTTGTATCAGGCTCGGACCAAGCTCTGCAGAACTCATTCCTTGTGAGACAG 1575
 Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGlnArgIleHisIleLeuLeuGlu 351
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 Db 1696 CTGGGGCCCTGTGTCTTGTGCTGCTGGGTGCTGTGCTGCTGCTGCTGATGACAG 1755
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 Db 1756 CAGATGAAGCGAGAGAACTCACTGACTTCACAGACCAACCAACCCCTGTGCTTA 1815
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 Db 1903 AAAAAGACCTTTTCACTCCAGATGACCTCAGAGAGATGGGTATGATGGGGCCATCATC 1962

Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCystrpGlu 485
 Db 1963 TCACACCTTTCTGAAGATGGGATATTTCTCAGAGAGACCCATCCCTCGAAC- 2013
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 Qy 506 LeuGlnGlyLeuGlu-----IleGluProAlaLeuCystrpProLeuTyrValGlnLysThr 523
 Db 2068 TTGAGAGATGAGAGGGGAGAGATTAACATTTCAATTGCAATCAATGATTTGGAAAAGACG 2127
 Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
 Db 2128 CTGAAGCA-----TATGAAATATACATGGCCTGTTGGGGCATCA 2166
 Qy 541 MetLysArgPheLeuPheGlyLeuValSerGlnAspValArgArgProLeuGlnValLeu 560
 Db 2167 ACCACAGTTCCTATTTGGGCTGTATGATGAGGGGAGAGAGAGATGAGAGACATC 2226
 Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
 Db 2227 TTTCACCTGCGGCTGTCTCAGGG----AGAACTGATGCAATGGATCCGCTCCTT 2280
 Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598
 Db 2281 CAGCTGTCTGCAGCCACAC-----TCTGTGAGTCCCTTCACATGC 2322
 Qy 599 LeuPheGlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsnSerPheGlnGlnVal 618
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 Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
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 Qy 679 GlnAspPheCysSerMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySer 698
 Db 2550 ----- 2550
 Qy 699 SerIleLeuThrGlnArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718
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 Db 2551 -----CAGATTTCTTTC 2562
 Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisIleLysLys 758
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 Db 2758 ----- 2758
 QY 919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIlyLeuLeuCysGlu 938
 Db 2761 ACCGAGCTGAGCCTGAGCTTCATGCTGCTCATGAGTGCCTGAGCCAAACACCTTTGCGCAG 2820
 QY 939 ValMetArgGluProSerCysHisLeuGlnAspLeuGlyLeuValIlyCysHisLeuThr 958
 Db 2821 AGACTGAGACAGCGAGCTGAGCTGAGCTACAGCAGCTGAGCTGAGCTGAGCTGAGCTGAG 2880
 QY 959 AlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuIlySerLeu 978
 Db 2881 TCTGACTGCTCCGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2940
 QY 979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnIlyLeuIlyS 998
 Db 2941 GACCTGAGCAGCAGAACCTGAGTGCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 3000
 QY 999 GlnIlyAsnSerValLeuThrArgLeuGlyLeuIlyValAlaCysGlyLeuThrSerAspCys 1018
 Db 3001 CATCTGCTGCAGAACTCATACGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 3060
 QY 1019 CysGlnAlaLeu-----SerLeuAlaLeuSerCysAsnArg 1030
 Db 3061 AGCGAGGAGCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
 QY 1031 HisLeuThrSerLeuAsnLeuValGln-----AsnAsnPhe 1042
 Db 3121 AAACCAAGTGTGATGACCCCTATTGAGGAGCTGAGTACCGGAGAGATGAGTAAATGACA 3180
 QY 1043 SerProIlyGlyMetMetIlyLeuCysSerAlaPheAlaCys-----ProThrSer 1059
 Db 3181 TCCCTCACTCAAGCGGAGGAGCTGAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
 QY 1060 AsnLeuGlnIleIleGlyLeuThrIlySerTrpGlnIlyProValGlnIleArgIlyLeuLeu 1079
 Db 3241 AATCTCAAACTCTGAGAGCTGAGCAAG--ATCTTCCCA-----ATTCTGAGAGTGA 3291
 QY 1080 GluGlu-----ValGlnLeuLeu--LysProArgValValIle 1091
 Db 3292 GAGGAAAGCTCCCGCAGAGGATGATACCGGTGGAATCTTGTGCGCTCTCTCTCTCTCTCT 3351
 QY 1092 AspGlySerTrpHisSer-----PheAspGluAsp----- 1101
 Db 3352 CAAGGAGAGCTGCATACGAAGCCTTTGGGAGCTGAGTGAATCTTCTGGGAGGAGGAGGAGG 3411
 QY 1102 -----AspArgHisIlyIleGlyLeuThrPheArgLeuProGlu 1114
 Db 3412 CCTGTGGCTACTGAGGATGATGACAAAGAAAGAACTT--GTACCGAGTTCATCTCCCTCT 3470
 QY 1115 SerArgAlaTrpProCysAlaLeuLeuThrGlyMetAsnProGlnIlyAlaIlyArgVal 1134
 Db 3471 AGCTGAGCTCTCAACCGCTGCGC-----CAACACGCGG 3500
 QY 1135 SerLeuLeuAlaGlyAspPheIlySerSerThrArgPheAlaIlySerLeuCysLeuAla 1154

Db 3501 TCTTGTCTTGTGTGTGAG--AGAAGCGGTGACCGTTGAGATTTGAATTTCTGTGTGTGGA 3557
 QY 1155 ThrAlaAsnGlyIlySerGlnArgValAspAsnValGluGlnSerSerProGlnProMet 1174
 Db 3558 CCAATCTCTGTGTGTGATCAA----- 3578
 QY 1175 AlaGlyThrGluHisIlyGlnAspIlyMetLeuSerValGlyTyrSerGlyAlaTrpSer 1194
 Db 3578 ----- 3578
 QY 1195 GluThrAlaGluLeuGlyIlyLeuGlySerAsnSerAlaAspHisLeuGlyIlyMet 1214
 Db 3579 CCCACAGCAGCAGCTGAGTGT--GCGAGGAGCTCTGTGAGATCAA-----GAGTGA 3629
 QY 1215 AlaTrpSerLeuGlyArgGluLeuSerSerArgIlyLeuCys-----ProThrValLeu 1232
 Db 3630 GCTTGGAGCCGTGA--AGCTGTGACACTCCCTTCATCTTGTGCTCTCCAAAGGG--GCC 3685
 QY 1233 MetThrThrAlaValCysProGlyHisIleTrpGluArgLeuGlySerArgIly----- 1249
 Db 3686 ATGTGACACATCCCTGT--TCCAGTGTGCCCATTTAAAGAGAGGAGATGCTCTGTG 3742
 QY 1249 ----- 1249
 Db 3743 AGAAGCCAGCAGGTGAGCTGATCATATGTTGTGAAACCAGCTTTTCCCT 3802
 QY 1250 -----Trp 1250
 Db 3803 TGGAGTCTCTGTAAATGATTCATATGCTGAGCTTATCCCTGACCTGTGTG 3862
 QY 1251 Cys-----LeuAsnSerAlaAspAsnHisSer----- 1259
 Db 3863 TGTGCTTTACACCGCTCCATCTGTAGAAAGTCACTTCCACTGATACCTGATCCAA 3922
 QY 1260 -----GlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlyIlyVal 1274
 Db 3923 GTGACTGCTCATTCGAGAAAGACTGAGC-----TGTGATATGAAAGCCCTGTGAG 3973
 QY 1275 SerAsnSerAlaAspAsnHisSerGlyValAla-----TrpSerLeuGlyAla-Ala----- 1291
 Db 3974 AAGACACTGTTCTCGAGTTCTACGTTGCGCACTTGGAGATCGAGATCGAGCTGCAAG 4033
 QY 1292 -----GlyLeuGluIlyLeu----- 1296
 Db 4034 TGAAGACAAAGATGAGACTGTGTGTGTGAGGCTTGTGTAACAGAGATGATCA 4093
 QY 1297 -----ValSerAsnSerAlaAspAsnHisSerIly-----ValSerTrpSerIle 1311
 Db 4094 TGCCTGCAACTGATCTGATTCCTCCAGCTGATGCGGTACCTTCACTTGTGATGCC 4153
 QY 1311 uGlyAlaAlaGlyLeuGlyIlyLeuValSerAsnSerAlaAspAsnHisSerGlyValIle 1331
 Db 4154 CGCAGTGTCTGCACTTGTGTGAGCAGATGACGAGCAGCTGATACCGAGTGAATCGG 4213
 QY 1331 rTrpSerLeu 1334
 Db 4214 -TGGAGTTG 4222
 RESULT 4
 US-11-136-527-4006
 ; Sequence 4006, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; PRIOR FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4006
; LENGTH: 4390
; TYPE: DNA
; ORGANISM: Rattus norvegicus
;
US-11-136-527-4006

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Alignment Scores:	
Prod. No.:	1 49e-22
Score:	354.00
Percent Similarity:	35.588
Best Local Similarity:	22.928
Query Match:	5.15%
DB:	8
	Gaps: 60
	Length: 4390
	Matches: 287
	Conservative: 171
	Mismatches: 454
	Indels: 342
	Indels: 360

US-10-066-521-6 (1-1344) x US-11-136-527-4006 (1-4390)

Qy	189	ThyValValLeuHisGlyIysSerCylIleGlyIysSerAlaAlaArgAlaIleVal	208
Db	1013	ACCAATCTTCATCCCTGGGTGATGATCGGGGTGGCAAGTCCATGATGCTACACGGCTGAG	10722
Qy	209	LeuCystrPAlaGlnGlyIleuTyrlGlnIlyMetPheSerTyrlValPhePheLeuPro	228
Db	1073	AGCCTCTGGGCGACGGGCGGCTAGACGACGGGCTC---AAATCTCTTCCATTTCCG	1129
Qy	229	ValArgLeuMetGlnArgIylsYlGlyIysSer-----ValThrGlnPheIleSer	245
Db	1130	TGCGCGATGTTTCAGCTGCTTCAGAGAAATGACAGAGCTGTCTCTGACGAGACCTCTCTTC	1189
Qy	246	ArgGlnIyrP-----ProAspSerGlnAlaProValThrGlnIleMetSerArg	261
Db	1190	AAGCACTACCTCTCTACCCAGACGGGAGCCCGACGAGAGGTGTTGGCTCTCTCTGCTTC	1249
Qy	262	ProGlnArgLeuLeuPhePheIleIleAspGlyPheAspPheLeuGlySerValIleuAsn	281
Db	1250	CCCCACGCGGCGCTTCTTCACTTCGATGCGCTGACGACGTCGACATCGGACTTG---	1303
Qy	282	AspThrIylsLeuCyIylsAsp-----ThrAlaGlyIylsGlnProProPheThr	297
Db	1304	GACCTGAGCCGCGTCCGACAGCTCTGCCCCCTGG---GAGCTGCCACACCTCTGCTC	1360
Qy	298	LeuIleArgSerLeuLeuArgIylsValIleuLeuProGlnSerPheLeuIleValThrVal	317
Db	1361	TTGCTGGCCAACTGCTCTACGTGGGAGAGCTGTTCAAGGGGCGTACGACGTCTCTACACCC	1420
Qy	318	Arg-----AspValGlyThrGlnIylsLeuIylsSerGlnValIalSerProArgTyr	334
Db	1421	CGCAGAGCATCGAGGTCCCGCGACAGTTCTCGCGAAAGAGTG-----	1465
Qy	335	LeuLeuValAlaArgGlyIleSerGlyGlnArgIleHisLeu-----	348
Db	1466	---CTTCTCCGGGCGCTTCTCCCCAGC-----CACCTGCGCGCTATGACGAGAG	1513
Qy	349	---LeuLeuGlnArgGlyIleGlyIylsGlnIylsGlnIylsThrGlnIylsLeuArgAlaIleMet	367
Db	1514	ATGTTCCCCCAGCGGGCGGCTCGACAGACCGGCTCGAGCAG---CTGAG	1561
Qy	368	AsnAsnArgIylsLeuLeuAspGlnCyserGlnValProAlaValIylsSerLeuIleCyVal	387
Db	1562	GCCAAACCCCAACTGTGACGCTGTGCTGTGCC-----CTCTCTGTGCTGG	1609
Qy	388	AlaLeu-----GlnLeuGln	392
Db	1610	ATCATCTTCCGGTGTCTTCAGCACTTCCGTCGTCTTTGAAGGTCAACCAAGCTGCCC	1669
Qy	393	AspValValIylsYlGlyIysSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAla	412
Db	1670	GACTGCG-----ACATGACCTCGAGACAGATGTCTCTCTCG	1705
Qy	413	PheVal-----PheHisGlnLeuThrProArgGlyValIalValArgGlyCylsLeuAsn	429
Db	1706	GTACATGAGGTCACTTGTAAACAGATGAGGCCACAGCACTGGTGTGACCGG-----AAC	1759

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Db 2725 GATCACCGATGTCGAGCCAGTAGTCACCAAAATCTGGATGATGATCAAGAGGCTCAC 2784
Qy 748 gSerLeuAsnLeuGlyThrHisLeuLysGluLysPheValArgMetAlaCysGluAl 768
Db 2785 GCATCTTAACTGGGAAAAAACAATAACAAGTAAAGAGGAGATATCTGGCCCTGAC 2844
Qy 768 aLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuSerCysGlyLeuThrHis 788
Db 2845 TGTGAGACACAGCAAA----- 2860
Qy 788 sAlaCysPheTyLeuLysHisSerGlnIleLeuThrThrSerProSerLeuLysSerLeu 808
Db 2861 -----TCAACTCTGAGAGTTGG 2877
Qy 808 rLeuAlaGlyValAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVa 828
Db 2878 GATGTGGGCAATCAAGTTGGGATGAAGAGCAAAAGCCTTCGACAGGCTCTGCG-- 2935
Qy 828 lSerGlnCysAlaLeuGlnLysLeuIleLeuGluLysAspCysGlyIleThrAlaThrGlyCy 848
Db 2936 -AACACACCCAGCCTTGACCAACCTGATGCTTCGCCCAACGSCATCTCCACAGAGAGG 2994
Qy 848 sGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAs 868
Db 2995 AAAGAGCCTTGCGAGGCGCTTCGACAGACAACGCTCTCAAAATATCTGTGCTGACCCA 3054
Qy 868 nAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetAlaGluProHisCy 888
Db 3055 AAATCAATCTCAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTC--AACCA 3111
Qy 888 sSerLeuGlnArgMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLe 908
Db 3112 GACGTTAAAGCATTTATGCTTATTCAGAAATCAAGATCAACAGTAAAGGAGCTGCCACGT 3171
Qy 908 uAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProVa 928
Db 3172 GCGAGATGCTTAAAGAGCAACATCGGCATACAGAGATTGCTTAATGAAACCTGAT 3231
Qy 928 lGluAspAsnGlyValLysLeuLeuCysGlyValMetArgGluProSerCysHisLeuGlu 948
Db 3232 AAAACACAGAGAGCGCAAAAGTCTAT--GAAATGATGAAGACGATATCTGTTTCTGAGA 3288
Qy 948 nAsp-----LeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSe 964
Db 3289 GGATCTTCTCTGTCATGAGGGTTTGGCTTCGAGCCTCAGACCAAAATGCACTTCG 3348
Qy 964 rLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAl 984
Db 3349 GCAATCTTTGTGTCAAGTGTCTTAAAGGGCCTGGCGAGGGGAGCTATCAGAGATCCAC 3408
Qy 984 aLeuGlyAspGlyGlyValAlaAlaLeuCys-GluGlyLeuLysGlnLysAsnSerValL 1004
Db 3409 TGCCCTCATGATGACAGCAAGCTTCCTGTCAGAAAGTCTGTGTCGCAAA-----C 3459
Qy 1004 eutThrArgLeuGlyLeuLysAlaCysGly-----LeuThrSerAspCysCys---- 1019
Db 3460 TCCCTAAGTACCCGCTACATTCCTGACAAAAAAGATGTCTCTGAGACTGTGATGTT 3519
Qy 1020 -----GluAlaL 1022
Db 3520 ACAATTAATACACTGTGAAGAGACTTATGCTATTAATATTTTATTCGAAGCTA 3579
Qy 1022 eusSerLeuAlaLeuSerCysAsnArg-----HisLeuThrSerLeuAsnLeuV 1038
Db 3580 GAGGATTAAGCTGTGAGCAAAACAGAGAGGCGACGCTCACTCATTCACAGACCTGCCA 3639
Qy 1038 aGlnAspAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProT 1058
Db 3640 TAGGACCAACGAGGAGC-----GAGTTGCTACCGCTCTTTTC----- 3677
Qy 1058 hSerAsnLeuGlnIleLeuGlyLeuTrpLysTrpGlnTrpProValGlnIleArgVal 1078

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Db 3678 -----ATTGAAGAGTTGAGATGCG-----CACAAAGTTGCT---GCCAAGC 3717
Qy 1078 eLeuGlu-----GluValGlnLeuLeuLys----- 1086
Db 3718 TTCTTGAATTAAGCTGTGATGATGATTAATTAATTAATTAATTAATTTCTCTCTC 3777
Qy 1087 -----ProArgValValIleAspGlySerTrpHisSerPheAspGluAspArgH 1104
Db 3778 AGCACTTCCCAT--GTATGTGATACGTGTCGCCACTTCACAGCTCG-----AGAC 3824
Qy 1104 lLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuT 1124
Db 3825 ACCGAGATATGTCAGTGGAGATTTGACTCTCCAG-----GTTTGT 3869
Qy 1124 rPglMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysSerS 1144
Db 3870 CGAAAGTTAATGTCAAGAAAGATGACACAGCGCTTTAATTTAATTCCTGAGTCTC 3929
Qy 1144 eThrArgPheAlaLysSer-----Leuc 1152
Db 3930 ACTGTCTCTGGCAAAAGATGAGATGAGATGCCCTCAGCTCTTACCTGTCTAAGATGACAT 3989
Qy 1152 yLeuAlaThrAlaAsnGlyGluSerGlnArgValAspAsnValGluGlnSerSerProG 1172
Db 3990 GCTTCAAAATGCT--GCTTCACCTCAGGCTTCTCTGCTAGCTACCTCTCTCTA 4046
Qy 1172 lProMetAlaGlyThrGluHisLys-----GlnAspLysMetLeuSerValG 1188
Db 4047 GAAAGCTAGTACCAATGAGGCTTACACTGTCTGCTGGGAAAGATGATGTCTCTCC 4106
Qy 1188 lTyTrSerGlyAlaTrp----- 1193
Db 4107 AAAGAAATAGGCAATGAGCTGCTGCCCTGAGCCCTGACATCCAAATGCGCTTTGTCTC 4166
Qy 1194 -----SerGluThrAlaGlu-----LeuG 1200
Db 4167 CCTTACTCTGTGAAGAGGAGAGTCTCTTCTGCTCCAGACACTAAGGCTGATCA 4226
Qy 1200 lGlyL-----LeuGlySerAsnSerAlaAspHis--AspHisG 1212
Db 4227 ACGGCGCGACAGATCAGAGGATGCGCTTGGAACTGGGCGCAGACAGCATGTGGACACC 4286
Qy 1212 lGlyMetAlaTrpSerLeuGly-----ArgG 1221
Db 4287 CCCACCAATGAGGCTGTGTGCTGCTGCTCATGAGGAGTGGGCTGATCTAGATC 4346
Qy 1221 lLeuSerSerArgGlyLeuCysProThrVal 1231
Db 4347 ACTTGTCTCT-----TGCCCGCTCAT 4369

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RESULT 5
 US-10-966-846-1
 / Sequence 1, Application US/10966846
 / Publication No. US20050287612A1
 / GENERAL INFORMATION:
 / APPLICANT: Bertin, John
 / APPLICANT: Philpott, Dana
 / APPLICANT: Sansonetti, Philippe
 / APPLICANT: Girardin, Stephen
 / TITLE OF INVENTION: CARD-4 MOLECULES AND USES THEREOF
 / FILE REFERENCE: 07334-371004
 / CURRENT APPLICATION NUMBER: US/10/966,846
 / CURRENT FILING DATE: 2004-10-15
 / PRIOR APPLICATION NUMBER: US 10/706,857
 / PRIOR FILING DATE: 2003-11-12
 / PRIOR APPLICATION NUMBER: US 10/352,381
 / PRIOR FILING DATE: 2003-01-27
 / PRIOR APPLICATION NUMBER: US 10/154,485
 / PRIOR FILING DATE: 2002-05-22
 / PRIOR APPLICATION NUMBER: US 10/027,881
 / PRIOR FILING DATE: 2001-12-20
 / PRIOR APPLICATION NUMBER: US 60/258,724
 / PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 3
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 3382
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (245) ... (3103)
 US-10-966-846-1

Alignment Scores:
 Pred. No.: 2,566-22 Length: 3382
 Score: 359.50 Matches: 225
 Percent Similarity: 38.30% Conservative: 135
 Best Local Similarity: 23.94% Mismatches: 367
 Query Match: 5.08% Indels: 214
 Gaps: 41

US-10-066-521-6 (1-1344) x US-10-966-846-1 (1-3382)

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 QY 209 LeuCystrPalaGlnGlyLysLeuTyrgInGlyMetPheSerTyrrValPhePheLeuPro 228
 Db 893 AGCCTTGCGGCGACGGGCGGCTGAGACGAGGGTCC--AAATCTTCTTCCACTTCCG 949
 QY 229 ValArgIleMetGlnArgLysLysGlySerSer-----ValTrpGlnPheIleSer 245
 Db 950 TGGCGCATGTTACAGCTGCTTCAAGAAAGTACAGCGGTGTGTGTCAGACGCTGCTTC 1009
 QY 246 ArgGluTrp-----ProAspSerGlnAlaProValThrGlnIleMetSerArg 261
 Db 1010 AAGCACTACTGCTACCCAGACGGGAGCCCGAGAGGAGTGTTCCTTCTGCTGCGCTTC 1069
 QY 262 ProGlnArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 281
 Db 1070 CCCACAGTGGCCCTCTTCACTTCACTTGAATGGCTGACAGCTGCACTGGACTTG----- 1123
 QY 282 AspThrLysLeuCyLysAsp-----TrpAlaGlnLysGlnProProPheThr 297
 Db 1124 GACCTGAGCGCGCGCTGACAGCTGCTGCGCTGCG-----GAGCTGCCACCCCTGATC 1180
 QY 298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSerPheLeuIleValThrVal 317
 Db 1181 TTGCTGGCCAACTGCTCACTGAGGAGAGCTGCTCAAGGGGCTGACCAAGCTGCTACAGCC 1240
 QY 318 Arg-----AspValGlyThrGlnLysLeuLysSerGlnValValSerProArgTyr 334
 Db 1241 CGCACAGGACATCAGAGTCCGCGCCAGATTCCTGCGGAGAAAGTGT----- 1285
 QY 335 LeuLeuValArgGlyLysSerGlyGlnGlnArgIleHisLeu----- 348
 Db 1286 ---CTTCTCGGGGCTTCTCCCGCAGC-----CACCTGCGCGCTATGCCAGAGG 1333
 QY 349 ---LeuLeuGlnArgGlyIleGlyLysGlnHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
 Db 1334 ATGTTCGCCGAGCGGCGGCTGACAGAGCGCTGCTGAGCCAG-----CTGAG 1391
 QY 368 AsnAsnArgGlnLeuLeuAspGlnCyseGlnValProAlaValGlySerLeuIleCyseVal 387
 Db 1382 GCCAACCCCAACTCTGACAGCTGTGTCTGTGCCC-----CTTCTTGTCTGG 1429
 QY 388 AlaLeu-----GlnLeuGln 392
 Db 1430 ATCATCTTCGCGTCTCCAGCACTTCGCTGCTTGAAGGTACACACACTGCGCC 1489
 QY 393 AspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAla 412
 Db 1490 GACTGC-----ACGATGACCCCTGACAGATGTCTCTCTGCTG 1525

QY 413 PheVal-----PheHisGlnLeuThrProArgGlyValAlaArgCyLysLeuAsn 429
 Db 1526 GTCACTGAGGTTCATCTGAACAGAGATGCAGCCAGCGAGCTGTGACGCG-----AAC 1579
 QY 430 LeuGlnGlu-----ArgValValLeuLysAspPheCyArg 441
 Db 1580 ACAAGCAGCCAGTGAAGACCTTCCAGCGCGCGCGGACACTGTGCTGCTGGGGCAG 1639
 QY 442 MetAlaValGlnGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMetVal 461
 Db 1640 GTGGCCCAAGCGGCGGCTGAGAGAGAGCTTGTGTCTTCAACCCAGAGAGAGTCCAGGCC 1699
 QY 462 GlnGlyLeuGlnGlyLysSerGlu-----LeuArgAlaLeuPheHisMetAsn 476
 Db 1700 TCGGCGCTGACAGAGAGACATGACAGCTGAGCTGGCTTCTGCGGGCTTGGCGAGCTGGC 1759
 QY 477 IleLeuLeuProAspSerHisCyseGlnGlyLysThrThrPhePheHisLysSerLeuGln 496
 Db 1760 ---CCCGGGGTGAC---CAGCAGTCTTATGATTTTTCACCTCACCTCCAG 1807
 QY 497 AspPheCyAlaAlaLeuTyrrTyrrValLeuGlu----- 507
 Db 1808 GCCTTCTTTACAGCTTCTTCTGCTGTGTGACAGCAGGGTGGCACTCAGAGCTGCTC 1867
 QY 508 -----GlyLeuGlnIle-GlnProAlaLeu----- 515
 Db 1868 AGGTTCCTCAGAGTGAATGCCCTGCGGGGACAGCACAGTCTCTATCTTCC 1927
 QY 516 -----CyseProLeuTyrrValGlnLysThrLysArgSerMetGluLe 529
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 QY 529 LysGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuVal 549
 Db 1988 -AAGAA-----CACTTCCAGTTTACCAACTCTTCTGTGCGGGCTGT 2031
 QY 549 LysGlnAspValArgArgProLeuGlnValLeuLeuGlyCyseProValProLeuGlyVal 569
 Db 2032 GTCCAAAGCCAAACAGAAAGTCTGCGGCACTGTGTCGCCGCG--GCAAGCTGAGAG 2088
 QY 569 LysGlnLysLeuLeuHisIleTrpValSerLeuLeuGlyGlnGlnProAsn-----AlaThr 587
 Db 2089 AAGCGCAGAGCCCTG---TGGGCACACTGTTTTCAGAGCTGCGGGGCTTACCTGAAG 2145
 QY 587 rTrhProGlyAspThrLeuAspAlaPheHis----- 597
 Db 2146 CTGCGCCCGGCTTCAAGTCCAAAGCTTCAACACAGGTGACAGCCATGCCACGTTATCTG 2205
 QY 598 -----CyseLeuPheGlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsn 614
 Db 2206 GATGCTGCGCTGATCTTACAGAGACACAGAGCCAGAAAGTGGGCGACCTGGCGCCAGGGG 2265
 QY 614 rPheGlnGlnValTrpLeuProIleAsnGln-----AsnLeuAspLeuIleAl 630
 Db 2266 CATTCGCGCAACATCACTCAAGCTGACTGACAGCTGCTGCGGCCACATGACAGCGC 2325
 QY 630 AserSerPheCyLeuGlnHisIleCyseProTyrrLeuArgLysIleArgValAspValLysG 650
 Db 2326 CTTCTCTTGTCTGCTGATCACTTCTCC-----AAGCGGTGCGCTTACACTTACAGCA 2379
 QY 650 yIlePheProArgAspGlnSerAlaGlnAlaCyseProValValProLeuTrpMetArgAs 670
 Db 2380 CAACATCTCAAGACATACAGCGCGTGG-----GAGCTGAGGCGCTTCAAGCGCC-- 2431
 QY 670 pLysThrLeuIleGlnGlnGlnTrpGlnAspPheCyseMetLeuGlyThrHisProHis 690
 Db 2431 ----- 2431
 QY 690 sLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCy 710
 Db 2432 -CTCACTGTTCTGAGACTCAAGCTTAACAGATATGACGCTGGGTGAAGGTGCTTAAG 2490
 QY 710 sAlaLysLeuArgHisIleProThrCyLysLysIleGlnThr---LeuMetPheArgAsnAlaG 729


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Db      2491 CGAAGACTG-----ACCAATACAAATGTGACCTATTGGGTTTATACAAACCA 2544
Qy      729 nileThPro---GlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLeuAr 748
Db      2545 GATCGCCGATGTCCGAGCCAGATGATGACCAAAATCTGGATGATGATCAAGAGCCCTAC 2604
Qy      748 gserLeuAsnLeuGlyIleThrHisLeuLeuGlyIleValAspValArgMetAlaCysGluVal 768
Db      2605 GCATCTTTAACTGGGAAAAAACAATAACAGTGAAGAGGAGGAGATCTCGCCCTGAC 2664
Qy      768 aleuLeuHisIleProLysCysLeuLeuGlnSerLeuArgLeuAspCysCysGlyLeuThrHis 788
Db      2665 TGTGAAGAACAGCAAA----- 2680
Qy      788 sAlaCysIleLeuLysIleSerGlnIleLeuThrHiserProSerLeuLysSerLeuSe 808
Db      2681 -----TCATCTCGAGGTTGG 2697
Qy      808 rLeuAlaGlyValAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVa 828
Db      2698 GATGTGGGCAATCAAGTTGGGAGTGAAGAGCAAAACCTTCGAGAGGCTTCGCG-- 2755
Qy      828 lSerGlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAlaThrGlyCy 848
Db      2756 -AACCAACCCAGCTTGACCACTGATGCTTCGCTCAACGCGATCTCCAGAGAGAGG 2814
Qy      848 sGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAs 868
Db      2815 AAGAGCGCTTCGAGGCGCTCGACAGACACGCTCTTAGAATAATCGTGGCTGACCA 2874
Qy      868 nasSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCy 888
Db      2875 AATGAATCTCAACATGAGTAGGCGAGAGAGTTGGCAAAATGTTGAAAGTC--AACCA 2931
Qy      888 sSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuThrAlaGlyCysGlyPheIe 908
Db      2932 GACGTTAAAGCATTTATGCTTATCCAGATCAAGATCAAGCTAAGGAGGACTGCCACCT 2991
Qy      908 uAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProVa 928
Db      2992 GCGAGATCGCTTTCAGAGCAACACCTGCAATACAGATTGCTGCTTAATGGAACCTGAT 3051
Qy      928 lGlnAspAsnGlyValLysLeuLeuCysGlyValMetArgLysProSerCysHisLeuGln 948
Db      3052 AAACACAGAGAGGCGCAAGGTAT--GAGATGAGAAAGCGGATTAATCTTTCTGAGA 3108
Qy      948 nasP-----LeuGlnLeuValLysCysHisLeuThrAlaAlaCysCysGluSe 964
Db      3109 GAGTCTCTTCCTGTTCAATGAGGCTTTTGGCCCTCGAGGCTCAGACAGAAATGCCACTGG 3168
Qy      964 rLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAl 984
Db      3169 GCAGCTTTTGTGTGATGCTTAAAGGGGCTCGGAGCGCGGAGCTATCAGAGATCCAC 3228
Qy      984 aleuGlyAspGlyGlyValAlaAlaLeuCys-GlnGlyLeuLysGlnLysAsnSerVal 1004
Db      3229 TGCCTTCATGATGACAGCGAGGCTTCCTGTCAGAAAGTGTGTCGCGCAA-----C 3279
Qy      1004 euthrArgLeuGlyLeuLysAlaCysGly-----LeuThrSerAspCysGly 1019
Db      3280 TCCTCAAGTACCCGCTACATTCGACAGAAAAAGAAATGTCTTCGAGCTTTGT 3335

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; FILE REFERENCE: 07334-371004
; CURRENT APPLICATION NUMBER: US/10/966, 846
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 10/706, 857
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 10/352, 381
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 10/154, 485
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 10/027, 881
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258, 724
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-966-846-3

Alignment Scores:
Pred. No.: 2,89e-21 Length: 2859
Score: 347.00 Matches: 204
Percent Similarity: 38.44% Conservative: 122
Best Local Similarity: 24.06% Mismatches: 321
Query Match: 4.91% Indels: 202
DB: 7 Gaps: 37

US-10-066-521-6 (1-1344) x US-10-966-846-3 (1-2859)
Qy      189 ThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleVal 208
Db      589 AACATCTTCACTCGGCGTGAATGATGCGGGTGGCAAGTCCATGCTCTGACAGGCGCTGAG 648
Qy      209 LeuCySTPAlaGlnGlyGlyLeuTyrglnGlyMetPheSerTyValPhePheLeuPro 228
Db      649 AGCCTCGGGCCAGCGGCGGCTGACAGCGAGGGTC--AAATCTTCTTCACTTTCGCG 705
Qy      229 ValArgGlnMetGlnArgLysLysLeuSerSer-----ValThrGlnPheIleSer 245
Db      706 TGCCTGATGTTCACTGCTTCAAGAGAAAGTGAAGAGCTGTGTCTGACAGACTGCTCTTC 765
Qy      246 ArgGlnTrp-----ProAspSerGlnAlaProValThrGlnLysMetSerArg 261
Db      766 AAGACATCTGTGTAACCCAGAGCGGAGCCCGAGAGAGGTGTTGCTCTGCTGCGCTTC 825
Qy      262 ProGlnArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsn 281
Db      826 CCCACGTGGCCCTCTTCACTTCATGCTGAGCTGAGAGCTGCACTCGACTTG----- 879
Qy      282 AspThrLysLeuCysLysAsp-----TrpAlaGlnLysGlnProProPheThr 297
Db      880 GACCTGACCCGCGTCTGACAGCTCTGCCCCCTG3--GAGCTGCCCACTCCCTGCTGC 936
Qy      298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSerPheLeuIleValThrVal 317
Db      937 TTGCTGGCACTCTCTCAAGTGAAGCTGTCAAGAGGGGCTGAGCAAGCTGTCAAGCC 996
Qy      318 Arg-----AspValGlyThrGlnLysLeuLysSerGlnValValSerProArgTy 334
Db      997 CGCACAGCATCAGAGGTCCCGCGCAAGTTCCTGCGAGAAAGGTG----- 1041
Qy      335 LeuLeuValArgGlyIleSerGlyGlnGlnArgIleHisLeu----- 348
Db      1042 ---CTTCTCGGGGCTTCTCCCGCAGC-----CACTCGCGCGCTATGCCAGAGG 1089
Qy      349 ---LeuLeuGlnArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
Db      1090 ATGTTCCCGGAGCGGCGCTGAGAGACCGCTGCTGAGCCAG-----CTGGAG 1137
Qy      368 AsnAsnArgGlnLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387

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RESULT 6
US-10-966-846-3
Sequence 3, Application US/10966846
Publication No. US20050287612A1

GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Philipott, Dana
APPLICANT: Sansonetti, Philippe
APPLICANT: Girardin, Stephen
TITLE OF INVENTION: CARD-4 MOLECULES AND USES THEREOF

Db 1138 GCCAACCCCAACCTCTGCAGCTGTGCTGTGCCC-----CTCTTCTGTGCTG 1185
QY 388 ALLeu-----GlnLeuGln 392
Db 1186 ATCATCTTCGGGTCCTTCAGCACTTCCTGCTCTTGAAGGCTTCACCAAGCTGCCCC 1245
QY 393 ASPValValGlyGlnSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAla 412
Db 1246 GACTGC-----ACGATGACCTGACAGATGTCCTTCCTGCTG 1281
QY 413 PheVal-----PheHisGlnLeuThrProArgGlyValAlaArgArgCysLeuAsn 429
Db 1282 GTCACGTAGGTCATCTGAGACAGAGATGCAGCCAGCAGCTGTGGACCG-----AAC 1335
QY 430 LeuGlnGlu-----ArgValValLeuLysArgPheCysArg 441
Db 1336 ACAAGCAGCCAGTCAGAGACCTTCACGCGCGGAGACACTGTGTCTGCTGGGGCAG 1395
QY 442 MetAlaValGlnGlyValThrAsnArgLysSerValPheAspGlyAspAspLeuMetVal 461
Db 1396 GTGGCCCAAGCGGGCAGAGAGAGAGAGCTTTGTCTTCAACCAAGAGAGGTGACAGCC 1455
QY 462 GlnGlyLeuGlyGlnSerGln-----LeuArgAlaLeuPheHisMetAsn 476
Db 1456 TCCGGGCTGAGAGAGAGACATGCAGCTGCGCTTCCGCGGCTTGGCGAGCTGGGC 1515
QY 477 IleLeuLeuProAspSerHisCysGlnGlnThrThrPhePheHisLeuSerLeuGln 496
Db 1516 -----CCCGGGGGGTGAC--CAGCAGCTTATGAGTTTTCACCTTCACCTTCAG 1563
QY 497 AspPheCysAlaAlaLeuThrTyTyValLeuGln----- 507
Db 1564 GCCTTCTTTACAGCTTCTTCTGTGTGAGACAGAGGAGGCACTCAGAGCTGCTC 1623
QY 508 -----GlyLeuGlnIle-GluProAlaLeu----- 515
Db 1624 AGGTTCTTCAGAGATGATGATCCCTTCGCGGGGACAGCAACGTCCTGTATCCTCCC 1683
QY 516 -----CysProLeuTyValGlnLysThrLysArgSerMetGlnLe 529
Db 1684 TTCTCTCCGTTCCAGCTCTGCAGGGGAGGTGTCGGCGGGAGAGACCTTTCACAAAC 1743
QY 529 LysGlnAlaGlyPheHisIleHisSerLeuMetLysArgPheLeuPheGlyLeuVal 549
Db 1744 -AAGAGT-----CACTTCAGTTACCAACCTTCTGTGGCGGGCTGT 1787
QY 549 LysGlnAspValArgArgProLeuGlnValLeuLeuGlyCysProValProLeuGlyVal 569
Db 1788 GTCCAAAGCCAAACAGAAACTCTGCGGCACTGTGTGCTCCGCG--GCAAGCCTCAGAG 1844
QY 569 LysGlnLysLeuLeuHisIleThrValSerLeuLeuGlyGlnGlnProAsn-----AlaThr 587
Db 1845 AAAGCGCAAGGCCCTG--TGGGCAACCTGTTTTCCAGCTCGGGGCTAAGGAG 1901
QY 587 rThrProGlyAspThrLeuAspAlaPheHis----- 597
Db 1902 CTGAGCCCGGTTGAGGTCCAAAGCTTCAACAGGTGACAGGCCATGCCCCAGTTCACTG 1961
QY 598 -----CysLeuPheGlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsn 614
Db 1962 GATGCTGCGGTGCTGCTACAGACAGAGACAGAGGTGGGAGGCGGCGGCGGCGG 2021
QY 614 rPheGlnGlnValThrLeuProIleAsnGln-----AsnLeuAspLeuIleAl 630
Db 2022 CATCTGGCCCAACTCACTCAAGCTGACTACTGCAAGCCCTGCTGGCCGACCTCAGCGC 2081
QY 630 AspSerPheCysLeuGlnHisCysProTyLeuArgLysIleArgValAspValLysGln 650
Db 2082 CCTCTCTTGGTCTGATCATCTTCCCC-----AAGGGGCTGCGCTTACAGCTAAGCAA 2135
QY 650 yLlePheProArgAspGlnSerAlaGlnAlaCysProValValProLeuThrMetArgAs 670
Db 2136 CAACAACTCTCAACGACTAAGCGGTGCGG-----GAGCTGAGGCTTGTCAAGCCGC-- 2187

QY 670 pLysThrLeuIleGlnGlnIntrGlnAspPheCysSerMetLeuGlyThrHisProH 690
Db 2187 ----- 2187
QY 690 sLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCy 710
Db 2188 -CTCACTGTCTCAGCTCAGCTTAACAGATCAGTACAGAGTGGGTGAAGTGTCTAG 2246
QY 710 sAlaLysLeuArgHisProThrCysLysIleGlnThr-----LeuMetPheArgAsnAlaG 729
Db 2247 CGAAGGCTE-----ACCAATACAAATTTGACCTTATTTGGGTTTACAAACCA 2300
QY 729 nIleThrPro-----GlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLeuArg 748
Db 2301 GATCACCGAGTGTGGAGCCAGGATACGTCACCAAAATCTGTGATGAAATGCAAGGCTCAG 2360
QY 748 gSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGlnAspValArgMetAlaCysGlnAl 768
Db 2361 GCATCTTAACTGGGAAACAAATTAACAGTGAAGAGGAGAAATGTCCTGCCCTGGC 2420
QY 768 sLeuLysHisProLysCysLeuLeuGlnSerLeuArgLeuAspCysCysGlyLeuThrHis 788
Db 2421 TGTGAAGACAGCAA----- 2436
QY 788 sAlaCysTyLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSe 808
Db 2437 -----TCAATCTGTAGGTTGG 2453
QY 808 rLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db 2454 GATGTGGGGCAATCAAGTTGGAGTGAAGAGCAAAAGCCCTTGGCAGAGGCTTGGCG-- 2511
QY 828 LysGlnCysAlaLeuGlnLysLeuIleLeuGlnAspGlyTyrIleThrAlaThrGlyCys 848
Db 2512 -AACCAACCCAGCTTGAACCACTTGAATCTTGGTGTGCAAGGATCTCCACAGAGAGG 2570
QY 848 sGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAs 868
Db 2571 AAAGAGCTTGCAGAGGCGCTTCAGACAGAAACAGTCTCTGAATACTGTGGTACCCA 2630
QY 868 nAsnSerLeuGlyAsnGlnGlyValLeuLeuLeuCysAspSerMetArgLeuProHisCys 888
Db 2631 AAATGAATCAAGATGAACTGGCAGAGACTTGGCAAAATGTGAAAGTTC--AACCA 2687
QY 888 sSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLe 908
Db 2688 GAGCTTAACCAATTATGCTTATCCGAATCAGATCAGCTTAAGGGAGCTGCCAGCT 2747
QY 908 uAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProVa 928
Db 2748 GCGAGATGCTTACAGAGCAACCTGSCATTAACAGAGATTGCTTAATGAAACCTGAT 2807
QY 928 lGluAspAsnGlyValLysLeu 935
Db 2808 AAAACCAAGAGAGGCCAAAGTTC 2829
RESULT 7
US-11-147-047-23
; Sequence 23, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoyang
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147, 047
; PRIOR FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221, 097
; PRIOR FILING DATE: 2002-09-06

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PRIOR APPLICATION NUMBER: PCT/US01/07143
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 3213
TYPE: DNA
ORGANISM: Homo sapiens
US-11-147-047-23

Alignment Scores:
Pred. No.: 6,64e-15 Length: 3213
Score: 280.00 Matches: 233
Percent Similarity: 37.39% Conservative: 157
Best Local Similarity: 22.34% Mismatches: 348
Query Match: 3.96% Indels: 308
DB: Gaps: 51

US-10-066-521-6 (1-1344) x US-11-147-047-23 (1-3213)
QY 191 ValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgAlaValLeuGlyCys 210
DB 634 ATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTGCTGCGACGCAATGGCCATGCTC 693
QY 211 ThrAlaGlnGlyGlyLeuTyrlin---GlyMetPheSerTyrlValPhePheLeuProAla 229
DB 694 TGGGCTCCCGAAGAGTGCAAGGCTCTGACCAAGTTCAAAATTCGTTCTTCTCCGCTC 753
QY 230 ArgGluMetGlnArgGlyLysSerValThrGluPheIleSerArgGluThrPro 249
DB 754 AGCAGGGGCCAG---GCTGACCTTTTGAACCCCTCTGTGATCACTCTG 801
QY 250 Asp-----SerGlnAlaProValThrGluIleMetSerArgProGlu 263
DB 802 GATATACCTGGCACATCAGAGACATTCATGCGCATCTGCTGAGCTGCGCAG 861
QY 264 ArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAspThr 283
DB 862 AGGGTTCTTTCTCTTGATGGCTACATGATTC-----AAGCCC 903
QY 284 LysLeuCysLysAspThrAlaGluLysGlnProPheThrLeuIleArgSerLeu 303
DB 904 CAGAACTGCCAGAA-----ATCGAAGCCCTGATA 933
QY 304 ArgLysValLeuLeuProGluSerPheLeuIleValThr----- 316
DB 934 AAGGAAACCAACCGCTTCAAGAAACATGCTCATCGCACCACTACCACTGAGTGGCTGAG 993
QY 317 ---ValArgAspValGlyThrGluLysLeuLysSerGlnValIleSerProArgTyrl 335
DB 994 CACATCGGAGATTGGTGC---CTGACTCTGAGTGGGGGATATGACAGAAAC 1047
QY 336 LeuValArgGlyLysSerGlyGluGlnArgIleIleLeuLeuGluAlaArgGlyIleGly 355
DB 1048 AGCCGCCAGGCTCATCCGAAAGTGTGATCAAGACCTTCTGAAAGCTGTGTGCTC 1107
QY 356 GlnHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAspArgGluLeuAspGln 375
DB 1108 CAATTCAGAAATCAGAGTGTGATGAGAAATCATG----- 1143
QY 376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspVal 395
DB 1144 ---AAGACCCCTCTTGTGTGCTCATCTGT---GCATCCAAATG----- 1185
QY 396 GlyLysSerValAlaProPheAsnGlnThrLeuThrGlnLeuIleAlaAlaPheValPhe 415

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DB 1186 GGTGAAGTGAAGTTCCACTCTCACACAAACACGGTGTTCAT-----ACCTTC 1236
QY 416 HisGlnLeuThrProAlaGlyValIleArgArgCysLeuAsnLeuGlnGluArgVal 435
DB 1237 TATATCTG-----TTGATACAGAAAAACAAACAAATTAAGGTGTGCT 1284
QY 436 LeuLysArgPheCysArg-----MetAlaValGlnGlyValThr 448
DB 1285 GCAAGTGACTTCAATCCGAGGCTGACCACTGTGAGACCTGAGCTGAGAGGTGTGCTC 1344
QY 449 AsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGlu 468
DB 1345 TCCCAAGATTGATTGCAACTGACAGAT-----GTGTCACGCTGATATGAG----- 1392
QY 469 LeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrl 487
DB 1393 -----GATGCTCTGTGCAACCTGGGCTCTCTGTAAATATATCA 1431
QY 488 -----TyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
DB 1432 GCTGAAGTTCAAGCCAAATATTAATTTCTTCAAGTCAATTCAGAGATGACAGCA 1491
QY 501 Ala-----LeuTyrlTyrlValLeuGlnGlyLeuGlnIleGluProAlaLeuCysProLeu 518
DB 1492 GAGCAAGACTCACAGATTATGACGCTCATGACGACAG----- 1533
QY 519 TyrValGlnLysThrLysArgSerMetGluLeuGlnAlaGlyPheHis----- 535
DB 1534 -----GAGGTGACCAAGGAAATGTGATTCGCAAAAT---GGTTTCAATTCGCAAT 1586
QY 536 ---IleHis---SerLeuThrMetLysArgPheLeuPheGlyLeuValSerGluAspVal 554
DB 1587 TACATCACTTATAGCAGCCTGCTCCGCTACACCTGTGGGTCATCTGTGAGACCAAG 1646
QY 554 GlyArgProLeuGlnValLeuLeu-----GlyCysProValProLeuGlyVal 569
DB 1647 GCGTGTATGAGACCTCGCAGACGTATCAACACGCTGCTCTGCGACATTTTCAT 1706
QY 569 LysGlnLysLeuLeuHisIleThrValSerLeuLeuGlyGlnGlnProAsnAlaThrThrPr 589
DB 1707 CGCCAAAGGCTCTC---TGAAGACAGAAATCTTTGCAAAAGTGAACCAACCACTGCA 1763
QY 589 OGlyAspThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspLysGluPheVal 609
DB 1764 GCAAGAAATTTGAAAGCCATAAACATC-----AATCTCTTGATGA 1805
QY 609 GlnValAlaLeuAsnSerPheGlnGluValThr-----LeuProIleAsnGlnLeu 627
DB 1806 GTGTGACATCATTTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAAATTTGA 1865
QY 627 sPheIleIleAsnSerPheCysLeuGlnHisCysProTyrlLeuArgValIleArgVal 647
DB 1866 AGCTT-----TCTTTCAAGTA-----AAACCTTATATAT 1895
QY 647 sPValLysGlyIlePheProArgAsp-----GluSerAlaGluAlaCysProValVal 664
DB 1896 CAATCAGGAAACATCCCGATTAATTTGACTCTTTGAAACATTTGGCCAAATTTG 1955
QY 665 -----ProLeuThrMetArgAspLys 672
DB 1956 AAGTGCCTGACATTCAATAATGAACTTTAATGGGAGAACTATGCTCATGAGAA 2015
QY 672 hTrIleIleGlnGlnGln---ThrGluAspPheCysSerMetLeuGlyThrHisProHis 691
DB 2016 GCTGCAAGAACACACAGGTG-----AATCCAAAT--- 2045
QY 692 ArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCysAla 711
DB 2046 -----GGAAGAGGCCCAAGAACTACATTC 2072
QY 712 LysLeuArgHisProThrCysLysIleGlnThrLeuMetPheAspValAlaGlnIleThr 731

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Db 2073 CAG-----CAGGGCTGATCTTT---GTCTTCAACTGAA 2105
Qy 732 ProGlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsp 751
Db 2106 GCAAGAAATTGAGA-CTCTGAGGTC-ACACTC-----CGGAATTTCAAGCAAGTTGAAT 2157
Qy 752 LeuGlyValThrHisLeuValSerValArgMetAlaCysGluAlaLeuValHis 771
Db 2158 -----MAGCAAGATATCAAGATATCTGGGGAATAATTCAGCTCT 2196
Qy 772 ProLeuCysLeuLeuGlnSerLeuArgLeuAsp-----CysCysGlyLeuThrHis 788
Db 2197 -----GCCACAGCCTCAGGCTCAATAAAGAGATCTGGTGTGGCTGGA 2244
Qy 789 AlaCysThrLeuValHisSerGlnIleLeuThrHisProSerLeuValSerLeuSer 808
Db 2245 AGC-----CTCAGTTGGTCTCAGACCTGTAAGAACATTATTCCTCATG 2292
Qy 809 LeuAlaGlyAsnValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db 2293 GTGGAAGCCAGTCCCTCACC-----ATAGAAGATGAGAGCAGATC 2334
Qy 829 SerGlnCysAla--LeuGlnValLeuIleLeuGlnAspCys-----841
Db 2335 ACATCTGTACAAACCTGAAGAACTGATATCATGACCTACAGAAATCAACGGCTCCG 2394
Qy 842 ---GlyLeuThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db 2395 GGTGGTCTGACT-----GACAGCTTGGGTAACTTGAAAGAC 2430
Qy 861 LeuThrHisLeuValSerAsnSerLeuGlyValGlnGlyValAsnLeuLeuValCys 880
Db 2431 CTTCACAAAGCTCATATGATGATACATAAGATGAAGATGAAGATGCTATTAACCTAGCT 2490
Qy 881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetCysLeuValCysHisLeu 900
Db 2491 GAAGGCTGAAA-----AACCTGAAGAAAGATGCTTATTTATTCAT- 2529
Qy 901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetCysGlyAsnSerTrpLeuThrHis 920
Db 2530 -----TTGACCCAC 2538
Qy 921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValValLeuLeuValCysGln 938
Db 2539 TTGTCT-----GACATGGAAGGGAATGATCATATGATCAAG 2577
Qy 939 ValMetArgGluProSerCysHisLeuGlnAspLeuValValValCysHisLeuThr 958
Db 2578 TCTCTGTCAAGTGAACCTGTGACCTTGAGAAATTCATATTAATCTCTGTCTGTCTCT 2637
Qy 959 AlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuValSerLeu 978
Db 2638 GCAAAATGCAAGTGAATCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCAATCTT 2697
Qy 979 AspLeuThrAspAsnAlaLeuGlyAspGlyValValAlaAlaLeuValCysGlnGlyLeuVal 998
Db 2698 GATTATTCAGAAATTTACTGGAAGAAAGATGAAGATGAGCTCTTCAATGATGATGAGC 2757
Qy 999 GlnValAsnSerVal-----1003
Db 2758 AGATGAACGCTGTAAGAACAGCTCAGCAGCTGATGCTGCCCTGGGCTGTGACGTGCA 2817
Qy 1004 -----LeuThrArgLeuGly 1008
Db 2818 GGCAGCCTGAGCAGCCTGTGAAACATTTGAGGAGAGCTCCCAACACTGTCAGACCTTGGG 2877
Qy 1009 LeuValAlaCysGlyLeuThrSerAspCysCysGlnAlaLeuSerLeuAlaLeuSerCys 1028
Db 2878 TTGAAAAAATCGAAGACTCAGAGATACAGAGATTTGAATTTTATAGTGCATTTTGGGAAG 2937
Qy 1029 Asn-----ArgHisLeuThrSerLeuValGlnAsnAsnPheSerProLeuGly 1046
Db 2938 AACCTCTGAAGAAATCTTCAGAGAGTTGAATTTGGCGGGAATCTGTGACAGCAGATGAGA 2997

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Qy 1047 MetMetLeuValLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeu 1066
Db 2998 TGGCTTCCCTTCAATGGGTGATTT-----GAGAAATCTTAAGCAATTAAGTCTT 3045
Qy 1067 TrpValSerTrpGlnTrp-----ProValGlnIleArgValLeu----- 1078
Db 3046 TTTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAATCAGAAACTTAGCCAA 3105
Qy 1079 -----LeuGlnGluValGlnLeuLeuValProArgValIle 1091
Db 3106 GTGTATTCAGATTAACTTTTTCGAAAGAGCTAAGCTCTGT- 3147
Qy 1092 AspGlySerThrHisSerPheAspGluAspAspArgHisLeuValGlyLeuThrPheArg 1111
Db 3148 -----GGGTGG---CAATTTGATGATGATGATCTCAGTGTATTAACAGGTGCTTTAAA 3198
Qy 1112 Leu 1112
Db 3199 CTA 3201

RESULT 8
US-11-145-631-3
; Sequence 3, Application US/11145631
; Publication No. US20060003409A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OR INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREK
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/11/145,631
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-631-3

Alignment Scores:
Pred. No.: 1,46e-14 Length: 3072
Score: 276.00 Matches: 232
Percent Similarity: 37.30% Conservative: 157
Best Local Similarity: 22.24% Mismatches: 349
Query Match: 3.90% Indels: 308
Gaps: 51

US-10-066-521-6 (1-1344) x US-11-145-631-3 (1-3072)
Qy 191 ValLeuHisGlyValCysSerGlyIleGlyValSerAlaLeuAlaArgArgIleValLeuVal 210
Db 496 ATCATTAAGAGGGAATGTGCAAGAGCAATCCACTGTGCGGACATTTGCCATCTC 555
Qy 211 TrpAlaGlnGlyLeuValTrpGln--GlyMetPheSerTrpValPhePheLeuProVal 229
Db 556 TGGGGCTCCGGAAGTGCAAGGCTGTGACCAAGTTCAAAATTCGCTTCTCCGCTC 615
Qy 230 ArgGluMetGlnArgValCysGlnSerValThrGluPheIleSerArgValTrpPro 249
Db 616 AGCAGGCGCCAG-----GGTGAACCTTTTGAAGAACCTCTGTGATCAACTCTCG 663
Qy 250 Asp-----SerGlnAlaProValThrGluIleMetSerArgProGlu 263
Db 664 GATTTACTTGCAACAATCAGAGAGAGACATTCATGCGCATGCGCTGGAAGCTGCGGAG 723
Qy 264 ArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThr 283

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Db 724 AGGGTCTTTCTTCTTGATGGTACATGAATTC-----AACCC 765
Qy 284 LyeLeuCyLeuSerTrpAlaGluValGlnProProthLeuLeuLeuSerLeuLeu 303
Db 766 CAGAACTGCCAGAA-----ATCGAAGCCCTGATA 795
Qy 304 ArgLeuValLeuLeuProGlnSerPheLeuLeuLeuLeuLeuLeuLeuLeuLeu 316
Db 796 AAGGAACACACCGCTTCAGAAACATGCTATCTGCACACTACACTAGCTGCTGAG 855
Qy 317 ---ValArgSerValGlyThrGluValLeuLeuSerGlnValValSerProArgTrpLeu 335
Db 856 CACATACGAGAGTTGGTCC-----CTGACTGAGGTGGGATATGACAGAAC 909
Qy 336 LeuValArgGlyLeuSerGlyGlnArgLeuLeuLeuLeuGlnArgGlyLeuGly 355
Db 910 AGCGCCAGGCTCATCCGAGAGTGTATCAAGAGCTTGTGAAGCTTGTGCTC 969
Qy 356 GlnHisGlnLeuThrGlnGlyLeuArgAlaLeuMetLeuSerLeuLeuLeuLeuLeu 375
Db 970 CAATTCAGAAATCAGAGTCTTACGAATTCATG----- 1005
Qy 376 CysGlnValProAlaValGlySerLeuLeuLeuValAlaLeuGlnLeuGlnAspValVal 395
Db 1006 ---AAGACCCCTCTTGTGGTCACTGTC---GCAATCCAGATG----- 1047
Qy 396 GlyGlnSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisValAlaPheValPhe 415
Db 1048 GGTAAAGTGGTTCACCTCCACACAAACAGCTGTTCAT-----ACCTTC 1098
Qy 416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlnGluArgValVal 435
Db 1099 TATATGTG-----TTGATTCAGAAAAACAAACATTAAGCTGTGCT 1146
Qy 436 LeuValArgPheCysArg-----MetAlaValGlnGlyValTrp 448
Db 1147 GCAGTACCTTCATTCGAGCTGAGCCAGACCTGAGACCTAGCTCGAGAGGTGTTC 1206
Qy 449 AsnArgLeuSerValPheArgGlyAspArgLeuMetValGlnGlyLeuGlnGlnSerGln 468
Db 1207 TCCCAAGATTGATTGCAAGTCAAGAT-----GTGTCAAGCTGAATGAG----- 1254
Qy 469 LeuValArgLeuPheHisMetAsnLeuLeuProArgSerHisCysGlnGlnTrp--- 487
Db 1255 ---GATGCTCTGCTGACAACTGGCTCTCTGTAATATATCA 1293
Qy 488 ---TyrThrPheHisLeuSerLeuGlnAspPheCysAla 500
Db 1294 GCTCAAGCTTCAGGCCAAATATTAATCTTTCACAGTCACTTCAGAGATGACAGCA 1353
Qy 501 Ala-----LeuTyrValLeuGlnGlyLeuGlnGlnGlnProAlaLeuCysProLeu 518
Db 1354 GACAGAAAGTCAACAGATTATGACCTGATGAGCCAG----- 1395
Qy 519 TyrValGlnGlyThrValArgSerMetCysLeuGlnGlnArgLeuHis----- 535
Db 1396 ---GAGTGCACCAAGGAGTGTATCTGCAAAAT-GGTTCACTTTCGACAT 1448
Qy 536 ---HisSerLeuTrpMetValArgPheLeuPheGlyLeuValSerGlnAspValAla 554
Db 1449 TACATCCATTAAGAGCTGCTGCTGATACACCTGGGTGATGTGGAAAGCCAG 1508
Qy 554 ArgProLeuGlnValLeuLeu-----GlyCysProValProLeuGlnVal 569
Db 1509 GCGTGTATGAAGCTCGAGAGTGTATCAACAGAGCTGCTTCGAGCTTTCAT 1568
Qy 569 LysGlnLeuValLeuHisTrpValSerLeuLeuGlnGlnProAlaValThrTrp 589
Db 1569 GCGCAAGAGCTCTC---TGAGACAGAACTTTCGAAAGTGAAGAAACACCTGGA 1625
Qy 589 GlnValArgThrLeuValArgLeuHisCysLeuPheGlnThrGlnArgValGlnPheValAla 609
Db 1626 GCAAGAAATTCGAAAGCATTAACATC-----AATCTCTTGTGGA 1667

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Qy 609 GlnAlaLeuAsnSerPheGlnGln-ValTrp-----LeuProLeuAsnGlnAsnLeu 627
Db 1668 GTGGCATTCATTTATATCAAGAGATACATCAATCAAGCTGAGCCAGAAATTTGA 1727
Qy 627 sPheLeuLeuAsnSerPheCysLeuGlnHisCysProTyrLeuValGlyLeuArgValAla 647
Db 1728 AGCTT-----TCTTCAAGGTA-----AAGCTTATATAT 1757
Qy 647 sPValValGlyLeuPheProArgAsp-----GlnSerAlaGlnAlaCysProValVal- 664
Db 1758 CAACCTAGGAAACATCCCGATTAATTATTAATCTTTCGAACATTGCCCCAATGTTC 1817
Qy 665 -----ProLeuTrpMetArgAspTrp 672
Db 1818 AAGTCTCTGACTTCATTAATCTGACTTTTATGGGGAGCATAGCTTCATGAGAAA 1877
Qy 672 hTrpLeuLeuGlnGlnGln-TrpGlnAspPheCysSerMetLeuGlnThrHisProHisLeu 691
Db 1878 GCGTCGAGAAAGACAGAGTGG-----AATCCCAT--- 1907
Qy 692 ArgGlnLeuAspLeuGlnGlnSerLeuLeuThrGlnArgAlaMetCysThrLeuCysAla 711
Db 1908 -----GAAAGAGGCCCAAGAACTTACATTC 1934
Qy 712 LysLeuArgHisProThrCysLeuLeuGlnThrLeuMetPheArgAsnAlaGlnLeuThr 731
Db 1935 CAG-----CAGGCTGTATCTTT---GTTCCTCACTGGA 1967
Qy 732 ProGlyValGlnHisLeuTrpArgLeuValMetAlaAsnArgLeuAspSerLeuAsn 751
Db 1968 GCAGAAATTCAGAG-CTCTGAGGTC-ACATC-----CGGATTCAGCAAGTTGTAAT 2019
Qy 752 LeuGlnGlyThrHisLeuValGlnGlnArgValAlaArgMetAlaCysGlnAlaLeuLeuHis 771
Db 2020 ---AAGCAAGATATACATATCTGGGAAATATTCAGCTCT 2058
Qy 772 ProLysCysLeuLeuGlnSerLeuArgLeuAsp-----CysCysGlyLeuThrHis 788
Db 2059 ---GCCAAGCTCAGAGCTGCAATTAAGAGATGCTGCTGAGTGGTGA 2106
Qy 789 AlaCysTyrLeuLysLeuSerGlnLeuLeuThrThrSerProSerLeuLysSerLeuSer 808
Db 2107 AGC-----CTCAGTTGCTCTGACACCTGTAAGAACATTTATCTTCATG 2154
Qy 809 LeuAlaGlnLeuLysValThrArgGlnGlyAlaMetProLeuSerAspAlaLeuVal 828
Db 2155 GTGAAAGCCAGTCCCTCAC-----ATAGAAGATGAGAGCAGCATC 2196
Qy 829 SerGlnCysAla-----LeuGlnLeuLeuLeuGlnAspCys----- 841
Db 2197 ACATCTGTAAACAACTGAAACCTTGAAGTATTAATCACTCAAGATCAACAGCTGCG 2256
Qy 842 ---GlyLeuThrAlaThrGlnCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db 2257 GGTGCTGACT-----GACAGCTTGAGTAACTTGAAGAC 2292
Qy 861 LeuThrHisLeuCysLeuSerAsnSerLeuGlnArgGlnGlyValAsnLeuLeuCys 880
Db 2293 CTTCAAGCTCAATAGATGATTAAGATTAAGATGAAGATGCTATTAATTAACCT 2352
Qy 881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
Db 2353 GAGAGCTGAAA-----AAGCTTAAGATGTATTAATTCAT----- 2391
Qy 901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
Db 2392 -----TTGACCCAC 2400
Qy 921 LeuSerLeuSerMetAsnProValGlnAsp-----AsnGlyValValLeuLeuCysGln 938
Db 2401 TTGCT-----GACATGAGAGGAAATGATTAATCAATGTACAG 2439

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QY 939 ValMetArgGIubProSerCysHsIleuGlnAspLeuGluValIysCysHsIleuThr 958
Db 2440 TCCTGTGCAAGTAAACCCCTGTGACCTTGAAGAAATTCATTTAGCTCTCTCTCTCTCT 2499
QY 959 AlaAlaCysGluSerIleuSerCysValIleSerArgSerArgHsIleuLysSerLeu 978
Db 2500 GCAATGTGAGTAAATATCTAGCTCAGAAATCTTCACAATTTGGCTCAAACTGACCATTTCTT 2559
QY 979 ArgLeuThrAspMetAlaIleuGlyAspGlyGlyValAlaIleuCysGluGlyLeuLys 998
Db 2560 GATTTATCAGAAAATTAATCTGGAAGAAAGATGAATGAAGCTCTTCATGAACGTGATGAC 2619
QY 999 GlnLysAsnSerVal----- 1003
Db 2620 AGCATGAACCTGCTGAAGAACGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCA 2679
QY 1004 -----LeuThrArgGlyLeu 1008
Db 2680 GGCAAGCTGAGCAGCCCTGTGAAACATTTGGAGAGAGGTCCACAACTGTCGAAGCTTGGG 2739
QY 1009 LeuLysAlaCysGlyLeuThrSerAspCysGluAlaLeuSerIleuAlaLeuSerCys 1028
Db 2740 TTGAAAACTGAGAGACTCACAGATACAGAGATTGAATTTAGTGCAATTTTGGAAAG 2799
QY 1029 Asn-----ArgHsIleuThrSerLeuAsnLeuValGlnAsnAspSerProLysGly 1046
Db 2800 AACCTCTGAAAAAATCTCCAGCAGCTTGAATTTGGCGGAAATCGTGAGCAGATGGA 2859
QY 1047 MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeu 1066
Db 2860 TGGCTTCCTTCATGCGGTGATTT-----GAGAACTCTTAAGCAATTAGTGT 2907
QY 1067 TrpLysTrpGlnIly-----ProValGlnIleAspGlyLeu----- 1078
Db 2908 TTGACTTATAGTACTAAAGATTCTACCTGATCCAGCATTAAGTCAGAAACTTAGCCAA 2967
QY 1079 -----LeuGluGluValGlnLeuLeuLysProArgValAlaIle 1091
Db 2968 GTGTTATCCAGTTAACTTTTCTGCAAGAAAGCTAGCGTTGT----- 3009
QY 1092 AspGlySerTrpHsSerPheAspGluAspArgHsIlyValIleGlyLeuThrPheArg 1111
Db 3010 -----GGGTGG---CAATTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA 3060
QY 1112 Leu 1112
Db 3061 CTA 3063

RESULT 9
US-11-136-527-4003
; Sequence 4003, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4003
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4003

Alignment Scores:
Pred. No.: 1,51e-14 Length: 3133
Score: 276.00 Matches: 232
Percent Similarity: 37.30% Conservative: 157

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Best Local Similarity: 22.24% Mismatches: 349
Query Match: 3.90% Indels: 308
Db: 8 Gaps: 51

US-10-066-521-6 (1-1344) x US-11-136-527-4003 (1-3133)
QY 191 ValLeuHsIleLysSerGlyIleGlyLysSerAlaLeuAlaArgIleValIleuCys 210
Db 531 ATCATTTGAAGGGGAATCTGGCAAGCAAGATTCACCTGTGTCAGGCAATTCAGCATCTC 590
QY 211 TrpAlaGlnGlyLeuTrpGln---GlyMetPheSerTrpValPhePheLeuProVal 229
Db 591 TGGGGCTCCGGAAAGTCAAGGCTGACCAAGCTTCAAAATTTGATCTTCTCCCTGCT 650
QY 230 ArgGluMetGlnArgLysLysGluSerValThrGluPheIleSerArgGluTrpPro 249
Db 651 AGCAGGGGCCAG-----GGTGAACCTTTTGAACCTCTGTATCAATCTCTG 698
QY 250 Asp-----SerGlnAlaProValThrGluIleMetSerArgProGlu 263
Db 699 GATATACCTGGCAATCAAGAGACAGACATTCATGCGCATGCTGTAAGCTGCGGAG 758
QY 264 ArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThr 283
Db 759 AGGGTCTTTCCTTCTTGAATGCTCAATGAATTC-----AGCCC 800
QY 284 LysLeuCysLysAspTrpAlaGluLysGlnProProPheThrIleuIleArgSerLeu 303
Db 801 CAGAACTGCCCAAA-----ATCGAAGCCCTGATA 850
QY 304 ArgLysValLeuLeuProGluSerPheLeuIleValThr----- 316
Db 831 AGGAAACCAACCGCTTCAAGAAACATGTCATGTCACCACTACCACTGAGTCTGAGG 890
QY 317 ---ValArgAspValGlyThrGluLysSerGluValAlaSerProArgTrpLeu 335
Db 891 CACATACGGCAAGTTTGGTGCC-----CTGACTGCTGAGGTGGGGATATACAGAAAGAC 944
QY 336 LeuValArgGlyLysSerGlyGlnArgIleHsIleuLeuLeuGluArgGlyIleGly 355
Db 945 AGCGCCAGGCTCTCATCCAGAAAGTCGATCAAGAGCTTGTGTAAGGCTTGTGCTC 1004
QY 356 GlnHsGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGln 375
Db 1005 CAATTCAGAAATTCAGGCTCTGAGGAATCTCATG----- 1040
QY 376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValVal 395
Db 1041 ---AGACCCCTCTCTTTGTGTCATCATCTGT---GCAATTCAGATG----- 1082
QY 396 GlyLysSerValAlaProPheAsnGlnThrLeuThrGlyLeuHsAlaAlaPheValPhe 415
Db 1083 GGTGAAGTGAAGTTCCACTCTCACACAAACAAGCTGTTCAT-----ACCTTC 1133
QY 416 HsGlnLeuThrProArgGlyValAlaArgArgCysLeuAsnLeuGluGluArgValVal 435
Db 1134 TATGATCTG-----TTGATTCAGAAAAACAACAACAACATAAAGGTGTGCT 1181
QY 436 LeuLysArgPheCysArg-----MetAlaValGluGlyValTrp 448
Db 1182 GCAAGTACTTCAATTCGAGCCTGAGCACTGTGAGAGACTTAAGCTCTGGAGGGTGTTC 1241
QY 449 AsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGlu 468
Db 1242 TCCCAACAAGTTTATTTTCAAGTCAAGAT-----GTGTCAGAGCGGAATGAG----- 1289
QY 469 LeuArgAlaLeuPheHsIleMetAsnIleLeuLeuProAspSerHsCysGluGluTrp--- 487
Db 1290 -----GATGTCCTGCTGACAACTGAGGCTCTCTGTAAATATATACA 1328
QY 488 -----TyrThrPhePheHsIleuSerLeuGlnAspPheCysAla 500
Db 1329 GCTCAAGAGTTCAAGCCAAAGTAAATTTCTTTCACAAAGTCAATTCACAGAGTACAGCA 1388

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Qy 501 Ala-----LeuTyrValLeuGluGluLeuGluProAlaLeuCyProLeu 518
Db 1389 GAGCAAGACCTGACAGCTTATTTGACCTGATACAGCCAG----- 1430
Qy 519 TyrValGluLeuValArgSerMetGluLeuValGluAlaGlyPheHis----- 535
Db 1431 -----GAGGTGACCAAGGGAATGCTTACCGAAGAAAT-GGTTTCATTGGGACAT 1483
Qy 536 ---IleHis-SerLeuThrMetLeuValArgPheLeuPheGlyLeuValSerGluAspValAr 554
Db 1484 TACATTCACCTTATGACAGCTGCTCCGGTACACCTGTGGTCATCTGGAGACACAG 1543
Qy 554 GATGProLeuGluValLeuLeu-----GlyCyProValProLeuGlyVa 569
Db 1544 GCGTGTATGAGGACCTCGGACAGAGTGTATCAACAGCGCTGCTTCCGACATTTCCAT 1603
Qy 569 LlyeGluLeuLeuLeuHisTyrValSerLeuLeuGlyGluGluProAlaIleThrPr 589
Db 1604 CGCCAAAGGCTCTC---TGAGACAGGAATCTTTCGAAAGTGGAAAACACACATCGA 1660
Qy 589 OGlyAspThrLeuAspAlaPheHisCyLeuPheGluThrGluAspValAr 609
Db 1661 GCAGGAATCTGAAGCCATGAACATC-----AATTCCTTGTAGA 1702
Qy 609 GLeuAlaLeuAsnSerPheGluGluValTyr-----LeuProIleAsnGluLeuAla 627
Db 1703 GTGTGGCAATCATTTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAGAAATTTGA 1762
Qy 627 sPLeuIleAlaSerSerPheCyLeuGluHisCyProTyrLeuArgHisIleArgValA 647
Db 1763 AGCTT-----TCTTCAAGTA-----AAAGCTTATAT 1792
Qy 647 sPValIleGlyIlePheProArgAsp-----GluSerAlaGluAlaCyProValVal 664
Db 1793 CAATCAGGGAACATCCCGATTAATTAATTAATTTGAAACATTTGCCAATGTGGC 1852
Qy 665 -----ProLeuThrMetArgAspTyr 672
Db 1853 AAGTCTCTGACATTCATTAAGCTGACTTTATGAGGAGACTATGAGCTGAGGAA 1912
Qy 672 hLeuIleGluGluGln-TyrGluAspPheCySerMetLeuGlyThrHisProHisLeu 691
Db 1913 GCGTCGACAGACACAGGTGC-----AATTCACAT--- 1942
Qy 692 ArgGluLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLeuThrLeuCyAla 711
Db 1943 -----GGAAGAGGCCCAAGAACTACATTC 1969
Qy 712 LysLeuAspArgHisProThrCyLeuValIleGlnThrLeuMetPheArgAspAlaGlnIleThr 731
Db 1970 CAG-----CAGGCTGTATCTTT---GTTCCTTCACTGAA 2002
Qy 732 ProGluValGlnIleLeuThrArgIleValMetAlaAspArgAspLeuAspSerLeuAsn 751
Db 2003 GCGAATTCAGGA-CTGTGAGGTC-ACATC---CGGAATTCAGCAAGTTGAAT 2054
Qy 752 LeuGlyGlyThrHisLeuLeuSerGluIleAspValArgMetAlaCyGluAlaLeuLysHis 771
Db 2055 -----AAGCAAGATATCATATCTGGGAAATATTCAGCTCT 2093
Qy 772 ProLysCyValLeuLeuGluSerLeuArgLeuAsp-----CyCyGlyLeuThrHis 788
Db 2094 -----GCCAAGAGCTCAGGCTGCMAATGAAGATGTGCTGTGCTGCA 2141
Qy 789 AlaCyTyrLeuLeuIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSer 808
Db 2142 AGC-----CTCAGTTGGTCTTCAGACACTGTGAAGACATTTATCTCTCATG 2189
Qy 809 LeuAlaGlyAspLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db 2190 GTGAAAGCAGTCCCTCAC-----ATAGAAGATGAGAGGACATC 2231

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Qy 829 SerGlnCyAla---LeuGlnLysLeuIleLeuGluAspCyS----- 841
Db 2232 ACATCTGTAAACAACCTGAAACCTTAGATATCATGATCAAGAAATCAACGCTGCG 2291
Qy 842 ---GlyIleThrAlaThrGlyCyGlnSerLeuAlaSerAlaLeuValSerAspArgSer 860
Db 2292 GGTGTCTGACT-----GACAGCTTGGGTAACTGAAGAAC 2327
Qy 861 LeuThrHisLeuCyLeuSerAspAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCyS 880
Db 2328 CTTCAAAGCTCATTAAGATATTAAGATGAATGAAGATGCTATTAACCTAGCT 2387
Qy 881 ArgSerMetArgLeuProHisCySerLeuGlnArgLeuMetLeuAsnGlnCyHisLeu 900
Db 2388 GAAGCTGAA-----AAGCTGAAGAAAGATGTATTATTCAT----- 2426
Qy 901 AspThrAlaGlyCyGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTyrLeuThrHis 920
Db 2427 -----TTGACCCAC 2435
Qy 921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValLysLeuLeuCyGlu 938
Db 2436 TTGTCT-----GACATTCGAGAGGGAATGATTAATCATGCTCAG 2474
Qy 939 ValMetArgGluProSerCyHisLeuGlnAspLeuGluLeuValLysCyHisLeuThr 958
Db 2475 TCTCTGCAATGAACCTGTGACCTTGAAGAAATTAATTAAGTCTCCTGCTGCTGTCT 2534
Qy 959 AlaAlaCySvGluSerLeuSerCyValIleSerArgSerArgHisLeuLysSerLeu 978
Db 2535 GCAATGACAGTGAAGAAATCTGACAGATCTCAATTCACATTTGGTCAAACTAGCATTTCT 2594
Qy 979 AspLeuThrAspAlaAlaLeuGlyAspGlyValAlaAlaLeuCyGluGlyLeuLys 998
Db 2595 GATTATCAAGAAATTAATCTGAAAGAAAGATGAAGCTTTCATGAACCTGATCAC 2654
Qy 999 GlnLysAsnSerVal----- 1003
Db 2655 AGATGAACCTGTAAGAAACACTCAGCGCATGATGCTGCGCTGAGCGTGAAG 2714
Qy 1004 -----LeuThrArgLeuGly 1008
Db 2715 GCGAGCTGACAGCTGTGAAACATTTGAGAGAGTCCCAACCTGTCAGAGCTTGG 2774
Qy 1009 LeuLysAlaCySvGlyLeuThrSerAspCySvGlyAlaLeuSerLeuAlaLeuSerCyS 1028
Db 2775 TTGAAGAACTGAGACTCAGATACAGAGATTGAATTTTAAAGTGCATTTTGGAAAG 2834
Qy 1029 Asn-----ArgHisLeuThrSerLeuAsnLeuValGlnAspAsnPheSerProLysGly 1046
Db 2835 AACCTCTGAAGAACTTCACAGACTGAATTTGGCGGAAATCGTGTGACAGATGGA 2894
Qy 1047 MetMetLysLeuCySerAlaPheAlaCyAspProThrSerAsnLeuGlnIleGlyLeu 1066
Db 2895 TGGCTGCTTCATGCGGTATTT-----GAGAATCTTAACCAATTAAGTGT 2942
Qy 1067 TyrLysTyrGlnTyr-----ProValGlnIleArgLysLeu----- 1078
Db 2943 TTGACTTTAGTAAAGAAATTTCTACCTGATCAGCATTAAGTGAAGAAATTCGCCAA 3002
Qy 1079 -----LeuGluGluValGlnLeuLeuLysProArgValValIle 1091
Db 3003 GTGTATTCAGATTAATCTTCTGCAAGAGTAGGCTTGT----- 3044
Qy 1092 AspGlySerTyrHisSerPheAspGluAspArgHisLysValIleGlyLeuThrPheArg 1111
Db 3045 -----GGGTGG---CAATTGATGATGATGATCTCAGTGTATTAACAGTGCCTTTTAA 3095
Qy 1112 Leu 1112
Db 3096 CTA 3098

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RESULT 10

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US-11-145-631-1
; Sequence 1, Application US/11145631
; Publication No. US2006003409A1
; GENERAL INFORMATION:
; APPLICANT: Bectin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 0734-32901
; CURRENT APPLICATION NUMBER: US/11/145,631
; PRIOR FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
; US-11-145-631-1

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Alignment Scores:
Pred. No.: 1,51e-14 Length: 3133
Score: 276.00 Matches: 232
Percent Similarity: 37.30% Conservative: 157
Best Local Similarity: 22.24% Mismatches: 349
Query Match: 3.90% Indels: 308
Gaps: 51

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US-10-066-521-6 (1-1344) x US-11-145-631-1 (1-3133)

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Qy 191 ValLeuHisGlySerGlyLeuGlySerLeuAlaArgArgIleValLeuCys 210
    ::::: ||||| ::::: |||||
Db 531 ATCATTAAGGGGAATTTGGCAAGGCAATTCCTGCGGCGCATGTCATGCTC 590
Qy 211 TTPAlaGlnGlyLeuTyrgln--GlyMetSerSerTyrglnPhePheLeuProVal 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 591 TGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCCTCTCTCCGCTC 650
Qy 230 ArgGluMetGlnArgGlySerGlySerSerValThrGluPheIleSerArgGluTrpPro 249
    ::::: ||||| ::::: |||||
Db 651 AGCAGGGCCCAAG-----GTTGACCTTTTGAACCTCTGTGATCAACTCTCG 698
Qy 250 Asp-----SerGlnAlaProValThrGluIleMetSerArgProGlu 263
    ||||| ||||| ||||| |||||
Db 699 GATTATACCTGGCAATCAAGAACAGACATTCATGCGCATGCTGAGAGCTGCGGCA 758
Qy 264 ArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAspThr 283
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 759 AGGGTCTTTCTTCTTGATGGCTACATGAATTC-----AAGCCC 800
Qy 284 LysLeuCysLysAspTrpAlaGluLysGlnProProPheThrIleArgSerLeuLeu 303
    ::::: ||||| ::::: |||||
Db 801 CAGAACTGCCCAAGAA-----ATCGAAGCCCTGATA 830
Qy 304 ArgLysValLeuLeuProGluSerPheLeuIleValThr----- 316
    ::::: ||||| ::::: |||||
Db 831 AAGGAAGAACACCGCTTCAAGAACATGCTATCTGTCATACATCACTGAGTGCCTGAG 890
Qy 317 ---ValArgAspValGlyThrGluLysLeuSerGluValValSerProArgTyrlieu 335
    ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db 891 CACATACGGCGAGTTTGGTGGC-----CTGACTGCTGAGGTGGGATATGACGAAGAC 944
Qy 336 LeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGly 355
    ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db 945 AGCCGCCAGGCTCTTCATCCAGAGAGTGTCTATCAAGAGCTTGTGAAGCTTGTGCTC 1004
Qy 356 GluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAspArgGluLeuLeuAspGln 375

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Db 1005 CAATTCAGAAATCCAGGTCTGAGGAATTCATG----- 1040
    ::||| ||||| ::||| |||||
Qy 376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValVal 395
    ::||| ||||| ::||| |||||
Db 1041 ---AAGCCCCCTCTTTGTGTGATCACTTG---GCAATCCAGATG----- 1082
Qy 396 GlyGluSerValAlaProPheAsnGlnThrThrGlyLeuHisAlaAlaPheValPhe 415
    ||||| ||||| ||||| |||||
Db 1083 GGTGAAGATGATTCACCTGACACACAAACAGCTGTTCAT-----ACCTTC 1133
Qy 416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal 435
    ::||| ||||| ||||| |||||
Db 1134 TATGATCTG-----TTGATACGAAAAACAAACAAACATTAAGGTGGCT 1181
Qy 436 LeuLysArgPheCysArg-----MetAlaValGluGlyValTrp 448
    ||||| ||||| ||||| |||||
Db 1182 GCAAGTACCTTCATTCGAGACCTGAGACCACTGAGACCTTACCTCGAGGGTGTCTC 1241
Qy 449 AsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlySerGlu 468
    ::||| ||||| ||||| |||||
Db 1242 TCCCAAGATTTGATTTGCAATCGCAGGAT-----GTGTCAGCGTGAATGAG----- 1289
Qy 469 LeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrg 487
    ::||| ||||| ||||| |||||
Db 1290 -----GATGTCCTGCTGACCACTGGGCTCTCTGTAAATATACA 1328
Qy 488 -----TyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
    ||||| ||||| ||||| |||||
Db 1329 GCTCAAGAGTTCAGCCCAAGTAATTAATTTTTCACAGTCAATTCAGAGATACACAGCA 1388
Qy 501 Ala-----LeuTyrglyValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeu 518
    ||||| ||||| ||||| |||||
Db 1389 GAGCAAGACTCAGCAGGTTATTGAGTGTCTCATGAGCCAGAG----- 1430
Qy 519 TyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHis----- 535
    ||||| ||||| ||||| |||||
Db 1431 -----GAGGTGACCAAGGGGAATGTGTACTTCCAGAAAT--GGTTTCCATTTCCGACAT 1483
Qy 536 ---IleHis--SerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlnAspValAla 554
    ||||| ||||| ||||| |||||
Db 1484 TACATTCATTTATAGCAGCTCTCCGCTACCTGTGGGTCTATCTGTGAAGCACAG 1543
Qy 554 GArgProLeuGluValLeuLeu-----GlyCysProValProLeuGlyVal 569
    ::||| ||||| ||||| |||||
Db 1544 GCGGTATAGAAAGACCTCCAGACAGTATCAACAGGCTGCTTCCGACTTTCAT 1603
Qy 569 LysGlnLysLeuLeuHisIleTrpValSerLeuLeuGlnGlnProAsnAlaThrThrPr 589
    ::||| ||||| ||||| |||||
Db 1604 CGCCAGAGGCTCTCTC---TGGAGACAGAAATCTTGCMAAGTGTGAAAAACACACTGGA 1660
Qy 589 OGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValAla 609
    ||||| ||||| ||||| |||||
Db 1661 GCAGAAATTTGAAAGCCATAACATC-----AATTCCTTTGTGGA 1702
Qy 609 GLeuAlaLeuAsnSerPheGlnGlu--ValTrp-----LeuProIleAsnGlnAsnLeuVal 627
    ::||| ||||| ||||| |||||
Db 1703 GTGCGCATCATTTATATCAAGAGTACATCAATTCAGCCCTGAGCCAAAGATTGGA 1762
Qy 627 sPheLeuIleAlaSerSerPheCysLeuGlnHisCysAspTyrglyLeuArgValAla 647
    ||||| ||||| ||||| |||||
Db 1763 AGCTT-----TCTTTCAAGGTA-----AAGCTTATATAT 1792
Qy 647 sPValLysGlyIlePheProArgAsp-----GluSerAlaGluAlaCysProValVal 664
    ::||| ||||| ||||| |||||
Db 1793 CAACTCAGGAACATCCCCATTAATTTATTTGACTTTTGAACATTTGCCCAATTGTGC 1852
Qy 665 -----ProLeuTrpMetArgAspLysTrp 672
    ::||| ||||| ||||| |||||
Db 1853 AAGTGTCTGGACTTATTAATGACCTTTATGGGAGGTATGCTTCAAGGAGAAA 1912
Qy 672 hIleGluIleGluGln--TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeu 691
    ::||| ||||| ||||| |||||

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Db      1913 GCCTGACGAGACACAGGTGG-----AATCCACAT--- 1942
Qy      692 ArgGlnLeuAspLeuGlySerSerIleLeuThrGluAlaMetLysThrLeuCyseAla 711
Db      1943 -----GGAGAGAGCCGCCAGAACCTTCATCTCC 1969
Qy      712 LysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731
Db      1970 CAG-----CAGGGCTGTATCTTT-----GTTCTTCAACTGGAA 2002
Qy      732 ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751
Db      2003 GCAGGAATTCAGGA-CTCTGGAGGTC-ACACTC-----CGGAAATTCAGCAAGTTGAAAT 2054
Qy      752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCyseGluAlaLeuLysHis 771
Db      2055 -----AAGCAGATATTCATATCTGGGAAAAATTTACAGCTCT 2093
Qy      772 ProLysCysLeuLeuGlnSerLeuArgLeuAsp-----CysCyseGlyLeuThrHis 788
Db      2094 -----GCCACAGCCTCAGCTGCAATAAAGACATGCTGCTGTGGCTGCA 2141
Qy      789 AlaCysTyrlLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSer 808
Db      2142 AGC-----CTCAGTTGGTCTCTCAGCACCTGTAAGAACATTTATCTCTCATG 2189
Qy      809 LeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db      2190 GTGGAAGCCAGTCCCTCACCC-----ATAGAAGATGAGAGGACATC 2231
Qy      829 SerGlnCyseAla---LeuGlnLysLeuIleLeuGluAspCys----- 841
Db      2232 ACATCTGTAAACAACTGAAAACCTTGATATCTATGACTTACAGATCAACGCGTCCG 2291
Qy      842 ---GlyIleThrAlaThrGlyCyseGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db      2292 GGTGCTCTGACT-----GACAGCTTGGTAACCTGAGAAC 2327
Qy      861 LeuThrHisLeuCyseLeuSerAsnAsnSerLeuGlyAsnGlyValAsnLeuLeuCyse 880
Db      2328 CTTACAAAGCTCATTAATGATTAACATAAAGATGAAGAAAGATGCTATAAATAACTACT 2387
Qy      881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
Db      2388 GAAGGCTGAAA-----AACCTGAAGAAAGATGTTTATTTTCAT----- 2426
Qy      901 AspThrAlaGlyCyseGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
Db      2427 -----TTGACCCAC 2435
Qy      921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValLysLeuLeuCyseGlu 938
Db      2436 TTGTCT-----GACATTTGAGAGGAGGAATGATTAACATAGTCAAG 2474
Qy      939 ValMetArgGluProSerCyseHisLeuGlnAspLeuGluLeuValLysCysHisLeu 958
Db      2475 TCTCTGTAAGTAAACCTGTGACCTTGAAGAAATTAATTAATGCTCTGCTGTGCT 2534
Qy      959 AlaAlaCysCyseGlnSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978
Db      2535 GCAATATGACGAAATATCTAGCTCAAGATCTTCAACATTTGTTGTTGCAAACTGAGCATTTCT 2594
Qy      979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCyseGluGlyLeuLys 998
Db      2595 GATTATATCAGAAAATTACTGTGAAGAAAGATGAAGAAAGATGAACTGATGCAAC 2654
Qy      999 GlnLysAsnSerVal----- 1003
Db      2655 AGGATGAACGTGTGAACAGCTCAACCGCATGATGCTGCTGGAGGCTGTGACCTGCA 2714
Qy      1004 -----LeuThrArgLeuGly 1008
Db      2715 GGCAGCCTGAGAGCCTGTTGAACATTTGAGAGAGTCCACAACTGCTGAAGCTTGGG 2774

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Qy      1009 LeuLysAlaCyseGlyLeuThrSerAspCyseGluAlaLeuSerLeuAlaLeuSerCys 1028
Db      2775 TTGAAAACCTGAGACCTCAGATTAACAGATTTGAATTTTATAGTCATTTTGGAAAG 2834
Qy      1029 Asn-----ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db      2835 AACCTGTGAAGAAATCTCCAGACAGTTGAATTTGGCGGAAATCTGTGACGACATGATGCA 2894
Qy      1047 MetMetLysLeuCyseSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu 1066
Db      2895 TGGCTTGCTTCATGAGGTGATTT-----GAGATCTTAAGCAATTTGCTTT 2942
Qy      1067 TrpLysTrpGlnTyrl-----ProValGlnIleArgLysLeu----- 1078
Db      2943 TTTAACCTTAAGTACTTAAGAAATTTCTACCTGATCCAGCATTAAGTCAGAAAATTTAGCCAA 3002
Qy      1079 -----LeuGluGluValGlnLeuLeuLysProArgValValIle 1091
Db      3003 GTGTTATCCAACTTAACCTTTCTGCAAGAACCTAGGCTTGT----- 3044
Qy      1092 AspGlySerTrpHisSerPheAspGluAspArgHisLysIleGlyLeuThrPheArg 1111
Db      3045 -----GGGTGG---CAATTTGATGATGATGATCTCAGTGTATTTACAGGTGCTTTAAA 3095
Qy      1112 Leu 1112
Db      3096 CTA 3098

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RESULT 11

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US-11-145-631-6
; Sequence 6, Application US/11145631
; Publication No. US200600034098A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/11/145,631
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-631-6

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Alignment Scores:

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Pred. No.: 1.9e-14 Length: 3612
Score: 276.00 Matches: 254
Percent Similarity: 37.03% Conservative: 193
Best Local Similarity: 21.04% Mismatches: 423
Query Match: 3.90% Indels: 340
DB: 8 Gaps: 56

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US-10-066-521-6 (1-1344) x US-11-145-631-6 (1-3612)

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Qy      17 CysLeuTyrlLeuLeuAspLysGluLubegInThrPheLysGluLeuLeuLysLys 36
Db      541 TGCTGCGAAGAGGTGAGCAGAGATGCTGCTGAGGATCATTCATGATTTTGAAG 600
Qy      37 SerSerGlnSerTrpThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGlu 56
Db      601 GGTTCAGAGTCC-----TGTAACTC----- 621
Qy      57 CysLeuAlaLeuLeuHisGlyTyrlTyrlGlyAlaSerLeuAlaTrpAlaThrSerIle 76

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Db 622 -----TTTCTTAATCCCTTAAGGAGTGG-----AACTAT 651
Qy Ser1IephGluAsnMetAspLeuArgThrLeuSerGluValAlaArgAspAspMetLys 96
Db 652 CCTCTATATTAGAGACTTGAATGACAAAGTTTGGAGAGACACAAATTTGGGTTCTTT 711
Qy Lys1IeSerGlnAlaMetGluGlnGluGluValAlaThrAlaAlaGluThrGluGlnGlu 116
Db 712 AACATCACCTCTTCTCTAATAGCTTTTTCATGACGATCAGAGAGAGACTTGGAGAT 771
Qy 115SerGlnAlaMetGluGlnGluValAlaThrAlaAlaGluThrGluGlnGluHis 136
Db 772 TTGGCTCAGAGATTAAAGCACTTGACCATACCCCACTTTTGAACCTTTATCCCTT 831
Qy 137 G1yG1yAspThrTrpAspTrpLysSerHisValMetThrLysPheAlaGluGluAsp 156
Db 832 GGGAGAGATATT---GACATTATTTTAACTTGAAGAACACCTTCACAGAACTGTCTTG 888
Qy 157 ValArgAspSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGly 176
Db 889 TGGAGAGAGACCAACACATCACCGGTGGAGAGCTGACCTGAAATGGCTCTGACAG 948
Qy 177 AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSer 196
Db 949 GCTCTTCAGAGC-----CCCTGCACATTTGAAGGGGAATCT 984
Qy 197 G1y1IeGlyLysSerAlaLeuAlaArgArg1IeValLeuGluSerTrpAlaGlnGlyLeu 216
Db 985 GGGAAAGGCAAGTCACTGTGCTGACAGCAATTCCTGCTGCGGCTCCGAAATGTC 1044
Qy 217 TyrGln---GlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
Db 1045 AAGGCTGTACCAAGTTCAATGCTGTCTTCTCTCCGTCCAGACAGAGGCCAG----- 1098
Qy 236 LysGluSerSerValThrGluPhe1IeSerArgGluTrpProAsp----- 250
Db 1099 -----GGTGCACCTTTTGAACCCCTGTGATCACTCTGTGATATACCTGGACAAATC 1152
Qy 251 ----SerGlnAlaProValThrGlu1IeMetSerArgProGluArgLeuAspPhe1Ie 269
Db 1153 AGGAAAGCAATTCATGCGCATCTGTCTGAAGCTGGGCGAGAGGTTCTTTCTCTT 1212
Qy 270 AspGlyPheAspAspLeuGlySerValLeuAsnAspThrLysLeuGluLysAspTrp 289
Db 1213 GATGGCTCAACATGAATTC-----AAGCCCAAGACTGCCCGCAGAA--- 1251
Qy 290 AlaGluLysGlnProPheThrLeu1IeArgSerLeuLeuAlaGlyValLeuLeuPro 309
Db 1252 -----ATCGAAGCCCTGATAAAGAAACCAACCGCTTC 1284
Qy 310 GluSerPheLeu1IeValThr-----ValArgAspValGly 321
Db 1285 AAGAACTGGCTCATGTCACCACTACACATGAGTCCCTGAGGCAATACGGAGTTTGGT 1344
Qy 322 ThrGluLysLeuLysSerGluValAlaSerProArgTrpLeuLeuValArgGly1IeSer 341
Db 1345 GCC-----CTGACTGCTGAGGTGGGAGATGACAGAAAGACAGCCGACCTCATC 1398
Qy 342 G1yG1yGlnArg1IeHisLeuLeuLeuGluArgGly1IeGlyGluHisGlnLysThrGln 361
Db 1399 CGAAGATGCTGTCAAGAGACTGTGAGGCTTGTGCTCAAAATTCAGAAATTCACAG 1458
Qy 362 G1yLeuArgAla1IeMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaVal 381
Db 1459 TGGCTTGAGGAATCTCATG-----AAGACCCCTCTCTTT 1491
Qy 382 GlySerLeuLeuLysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaPro 401
Db 1492 GTGGTCACTCACTTGT---GCAATCCAGATG-----GGTGAAGAGTCACTTCAC 1536
Qy 402 PheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArg 421
Db 1537 TCTCACACACAAACAGCTGTTCAT-----ACCTTCTATGATCTG----- 1578

Qy 422 G1yValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArg 441
Db 1579 -----TTGATACAGAAAACAAACACAAACATAAAGGTGTGCTCGATGATCTCATTCGG 1635
Qy 442 -----MetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
Db 1636 AGCTGGACCACTGTGAGAGACTTGTGAGAGGGTGTGTCTCCCAAGTTTGATTTTC 1695
Qy 455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474
Db 1696 GAACCTGAGGAT-----GTGTCAAGGTAAATGAG----- 1725
Qy 475 MetAsn1IeLeuLeuProAspSerHisCysGluGluLys----- 487
Db 1726 ----GATGTCTGTGACAACTGGGCTCTGTGAAATATACAGTCAAGGTTCAAGCCA 1782
Qy 488 ---TyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAla-----LeuTyrTrp 504
Db 1783 AAGTATTAATTTCTTTCAAGATTCATTCAGAGATACACAGACAGACATTCAGCAGT 1842
Qy 505 ValLeuGluGlyLeuGlu1IeGluProAlaLeuCysProLeuTyrValGlyLysThrLys 524
Db 1843 TTATGACGTCTCATGAGCCAGAG-----GAGGTGACCAAG 1878
Qy 525 ArgSerMetGluLeuLysGlnAlaGlyPheHis-----1IeHis-SerLeuTrp 540
Db 1879 GGGAGATGTTACTTGCAGAAAT---GGTTTCATTTCCGACATTTACATTCACCTATAGCAG 1937
Qy 540 PheLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLe 560
Db 1938 CCGTCTCCGGTACACCTGTGGTGCATCTGTGAAGCCACACAGGAGCTGTATGAAGACCT 1997
Qy 560 LysLeu-----GlyCysProValProLeuGlyVal1IeGlnLysLeuLeuHis 575
Db 1998 GCGACAGTATACACACAGGCTGTCTCTCGACATTTCCATGCGCAAGAGGCTTCTC-- 2055
Qy 575 ATTPValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAl 595
Db 2056 -TGGAGACAGAAATCTTTCGAAAGTGGAAGAAACACACATGACAGCAAGAAATTCGAAAGC 2114
Qy 595 ArgPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPh 615
Db 2115 CATTAACATC-----AATTCCTTTGAGAGCTGTGGCATTCATTTATA 2156
Qy 615 eGlnGlu-ValTrp-----LeuPro1IeAsnGlnAsnLeuAspLeu1IeAlaSerSerP 633
Db 2157 TCAAGAGATACATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTT-----TCTT 2207
Qy 633 heCysLeuGlnHisCysProTyrLeuArgLys1IeArgValAspValLysGly1IePheP 653
Db 2208 TCAAGGTA-----AAGCTTATATATACATCAAGGAAACATCCC 2246
Qy 653 LysArgAsp-----GluSerAlaGluAlaCysProValVal----- 664
Db 2247 GATTACTTATTTGACTTTTGAACATTTTGCCCAATTTGGCAAGTCCCTGCACTTCAT 2306
Qy 665 -----ProLeuTrpMetArgAspLysTrpThrLeu1IeGluGln- 677
Db 2307 TAAACTGACTTTTATGCGGAGACTATGCTTCATGGAAGAAAGCTGCACAAAGACAGG 2366
Qy 678 TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly 697
Db 2367 TGG-----AATCCACAT----- 2378
Qy 698 SerSer1IeLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuAspGHisProThr 717
Db 2379 -----GGAAAGAGGCCCAAGAACTTACATTTCCAG----- 2408
Qy 718 CysLys1IeGlnThrLeuMetPheArgAsnAlaGln1IeThrProGlyValGlnHisLeu 737
Db 2409 -----CAGGGCTGTATCTTT---GTTCCTCACTGGAAGACAGAAATTCAGGA-CTC 2455

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Qy 738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyThrHisIleu 757
Db 2490 TGGAGCTC-AACATC-----CGGATTTCAAGCAAGTGAAT-----
Qy 758 LysGluIleuValArgMetAlaCysGluIleuValSerProLysCysLeuLeuGlu 777
Db 2491 ---AAGCAAGATATCAGATATCTGGGAAATATTCACCTCT-----GCCACA 2535
Qy 778 SerLeuArgLeuAsp-----CysCysGlyLeuThrHisAlaCysTyrLeuValIle 794
Db 2536 AGCTTCAGGCTGCAGAAATTAAGAGATGCTGCTGTGGCTGAAGC-----CTC 2583
Qy 795 SerGlnIleLeuThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysVal 814
Db 2584 AGTTGGCTCTCAGACCTGTAAGAACATTTATTTCTTCATGCTGGAAGCCAGTCCCTC 2643
Qy 815 ThrArgGlnIleValMetProLysSerArgAlaLeuArgValSerGlnCysAla--Leu 833
Db 2644 ACC-----ATAGAGATGAGAGACACATCACAATCTGTAAACAACCTG 2685
Qy 834 GlnIleValLeuLeuGluAspCys-----GlyIleThrAlaThr 846
Db 2686 AAAACCTTGAGTATTCATGACCTTACAGATCAACGCTGCGGTGCTGACT----- 2739
Qy 847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
Db 2740 -----GACAGCTTGGGTAACTTGAAGAACCTTTCACAAAGCTCAATATG 2781
Qy 867 SerAsnAsnSerLeuGlyAsnGlnIleValAsnLeuValCysArgSerMetArgLeuPro 886
Db 2782 GATAACATTAAGATGATGAAGAGATGCTATAAATCAGTGAAGCCTGAAA----- 2835
Qy 887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
Db 2836 ---AACCTGAAGAGATGCTGTTATTCAT----- 2862
Qy 907 PheLeuAlaLeuAlaLeuMetClyAsnSerTrpLeuHisLeuSerLeuSerMetAsn 926
Db 2863 -----TTGACCCCACTTCTCT----- 2877
Qy 927 ProValGluAsp-----AsnGlyValLysLeuValCysGluValMetArgGluProSer 944
Db 2878 -----GACATTGAGAGAGGAGATGATTAATACATATGCAAGTCTCTCAAGTGAACCC 2928
Qy 945 CysHisLeuGlnAspLeuGlnLeuValLysCysHisLeuThrAlaAlaCysCysGluSer 964
Db 2929 TGTGACCTTGAAGAAATTCATTAATTAAGTCTCTGCTGCTGCAAAATGCAAGTGAATAATC 2988
Qy 965 LeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAla 984
Db 2989 CTAGCTCAGAAATCTTCACAATTTGCTCAAACTGAGCATTTCTTGATTTATCAGAAAATTAAC 3048
Qy 985 LeuGlyAspGlyGlyValAlaAlaLeuValCysGlnIleLeuValLysAsnSerVal--- 1003
Db 3049 CTGAAAAGAAATGAAATGAAGCTCTTCAATGAACATGACAGATGAAGTGGCTGAAGA 3108
Qy 1003 ----- 1003
Db 3109 CAGCTCACCGCAGCTGATGCTGCTGCGGCTGTGACGTGCAAGGAGCCTGACGACCTG 3168
Qy 1004 -----LeuThrArgLeuGlyLeuValAlaCysGlyLeu 1014
Db 3169 TTGAAACATTTGGAGAGAGGTCCCAACATCTGTCAGCTTGGGTGAAAACCTGAGACATC 3228
Qy 1015 ThrSerAspCysCysGluValAlaLeuSerLeuAlaLeuSerCysAsn-----ArgHisLeu 1032
Db 3229 ACAAGTACAGAGATTAAGATTTTAAAGTGAATTTTGGAAAGAACCTCTGAAAACATTC 3288
Qy 1033 ThrSerLeuAsnLeuValGlnAsnAsnLysSerProLysGlyMetCysLeuCysSer 1052
Db 3289 CAGCAGTGAATTTGGCGGGAATCTGTGAGCAGATGATGCGCTTCCCTTCAATGGGT 3348
Qy 1053 AlaPheAlaCysProThrSerAsnLeuGlnIleLeuGlyLeuTrpLysTrpGlnTyr--- 1071

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Db 3349 GATATT-----GAGAAATCTTAAGCAATTAAGTGTTTTGACTTAAGTAA 3396
Qy 1072 -----ProValGlnIleArgLysLeu----- 1078
Db 3397 GAATTTCTACTGATATCCAGCATTTGATGTCAGAAACTTACCCAAAGTTATCCAACTTA 3456
Qy 1079 ---LeuGlnGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSer 1097
Db 3457 TTTCTGCAAGAGAGCTGAGCTTGT-----GGGTGG---CAA 3489
Qy 1098 PheAspGluAspAsp 1102
Db 3490 TTTGATGATGATGAT 3504

RESULT 12
US-11-145-631-4
; Sequence 4, Application US/11145631
; Publication No. US2006003409A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/11/145, 631
; PRIOR FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841, 739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697, 089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161, 822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
; US-11-145-631-4

Alignment Scores:
Pred. No.: 1,91e-14 Length: 3615
Score: 276.00 Matches: 254
Percent Similarity: 37.03% Conservative: 193
Best Local Similarity: 21.04% Mismatches: 423
Query Match: 3.90% Indels: 340
DB: 8 Gaps: 56

US-10-066-521-6 (1-1344) x US-11-145-631-4 (1-3615)
Qy 17 CysLeuTyrGlnLeuAspLysGlnIlePheLysGlyLeuLeuValLys 36
Db 541 TGTCTCAGAGAGGTGAGACAGATGCTGTAGAGGATCATTCATGATTTGAAAAAG 600
Qy 37 SerSerGlnSerThrThrCysSerIleProGlnPheGlnIleGluAsnAlaValGlu 56
Db 601 GGTTAAGAGTCC-----TTTAACCTC----- 621
Qy 57 CysLeuAlaLeuLeuHisGlyTyrGlyAlaSerLeuAlaTrpAlaThrSerIle 76
Db 622 -----TTTCTTAATCCCTTAAGAGTGG-----AACTAT 651
Qy 77 SerIlePheGluAsnMetAsnLeuArgThrLeuSerGlyValAlaArgAspMetLys 96
Db 652 CCTTAATTCAGCACTTGAATGACAAAGTTTGAAGAGACACAGAAATTTGGCTTTCTTT 711
Qy 97 LysIleSerGlnAlaMetGlnGlnIleGlnIleAlaThrAlaAlaGluThrGlnGlnGln 116
Db 712 AACATCACCTCTCTTAATAGGTTTCTTATTCAGACATCAGAAAGAGACTTGACAT 771
Qy 1117 IleSerGlnAlaMetGlnGlnIleGlnIleAlaThrAlaAlaGluThrGlnGlnGln 136

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Db      772 TTGGCTCAGGATTTAAAGACTGTGACCATACCCCACTTTTCGACTTTTATCCCTT 831
Qy      137 GYGLVAspThrTrpAspTrpTyrLysSerHisValMetThrLysPheAlaGluGluAsp 156
Db      832 GGTGAAGATATTT---GACATTTATTTTAACTGTAAAGACACTTACAGAAACCTGCTCTG 888
Qy      157 ValArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGly 176
Db      889 TGGAGAGAGACCAACCATCAACCGGTGAGAGAGCTGACCGTGAATGCGCTCTGACAG 948
Qy      177 AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSer 196
Db      949 GCTCTTCAGAGC-----CCCTGCATCATTTGAAGGGGAATCT 984
Qy      197 GYVLeuLysSerAlaLeuAlaArgArgGLeuLeuLeuSerProAlaGlnGlyLeu 216
Db      985 GGCAGAAAGCAAGTCTGCTGTCGACCGAATTCGCTGCGGGCTCCGAAAGTGC 1044
Qy      217 TyrGln---GlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
Db      1045 AAGGCTGTGACCAAGTTCAATTCGTCTTCTCTCCCTCCGCTCAGCAGGCGCCAG----- 1098
Qy      236 LysGluSerSerValThrGluPheLeuSerArgGluTrpProAsp----- 250
Db      1099 ---GGTGAAGCTTTTGAACCCCTGTGATCAACTCTCGATATACCTGCGACATC 1152
Qy      251 ---SerGlnAlaProValThrGluLeuMetSerArgProGluArgLeuPheAlaLe 269
Db      1153 AGGAGACAGACATTCAATGCGCAGTCTGTAAAGCTCGCGCAGAGGGTCTTTTCTCTT 1212
Qy      270 AspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCybLysAspTrp 289
Db      1213 GATGGCTACATGATTC-----AAGCCCAAGAACTGCCAGAA--- 1251
Qy      290 AlaGluLysGlnProProPheThrLeuLeuArgSerLeuLeuArgLysValLeuLeuPro 309
Db      1252 -----ATCGAAGCCCTGATAAAGGAAACCAACCGCTTC 1284
Qy      310 GluSerPheLeuLeuValThr-----ValArgAspValGly 321
Db      1285 AAGAACTGGTCACTGTCACTACCACTACCACTGAGTCCCTGAGGACCATTAAGCACTTGGT 1344
Qy      322 ThrGluLysLeuLysSerGluValValSerProArgTrpLeuLeuValArgGlyLeuSer 341
Db      1345 GCC-----GTGACTGCTGAGGTGGGGATATGACAGAAAGACGGCCAGGCTCATC 1398
Qy      342 GlyGluGlnArgLysLeuLeuLeuGluLysArgGlyLeuGlyLeuHisGlnLysThrGln 361
Db      1399 CGAAGAACTGCTGATCAAGAGAGCTTGTGAAGGCTTGTGTCCAAAATTCAGAAATCCAGG 1458
Qy      362 GlyLeuArgAlaLeuMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaVal 381
Db      1459 TCGTGTGGAATTCATG-----AAGACCCCTCTCTTT 1491
Qy      382 GlySerLeuLeuCybValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaPro 401
Db      1492 GTGGTCACTCACTCT---GCAATCCAGATG-----GGTGAAGAGTCAATTCAC 1536
Qy      402 PheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArg 421
Db      1537 TCTCACACACAAACACACGCTGTTCCAT-----ACCTTCTATGATCTG----- 1578
Qy      422 GYValValArgArgCybLeuAsnLeuGluGluArgValValLeuLysArgPheCybArg 441
Db      1579 ---TTGATACAGAAACAAACACAAACATTAAGGTGGTGGCTGCAAGTCAATTCGCG 1635
Qy      442 -----MetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
Db      1636 AGCCTGAGCACTGTGAGACCTAGCTCTGAGAGGTGTGTTCTCCCAAGTTTGATTTTC 1695
Qy      455 AspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeuArgAlaLeuPheHis 474

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Db      1696 GAACTGAGAGAT-----GTGTCCAGCGTGAATGAG----- 1725
Qy      475 MetAsnLeuLeuProAspSerHisCybGluGluTyr----- 487
Db      1726 ---GATCTCTGTGTCACAACTGGGCTCTCTGTGAATATATACAGTCAAGATTCAAGCCA 1782
Qy      488 ---TyrThrPhePheHisLeuSerLeuGlnAspPheCybAlaAla-----LeuTyrTyr 504
Db      1783 AAGTATTAATTTCTTCACAAGTCAATTCAGAGATACACAGCAGACGAAAGCTTCAGCACT 1842
Qy      505 ValLeuGluGlyLeuGluGlnProAlaLeuCybProLeuLysValGlyLysThrLys 524
Db      1843 TYATATCTGTCAATAGCCAGAG-----GAGGTGACCCAG 1878
Qy      525 ArgSerMetGluLeuLysGlnAlaGlyPheHis-----IleHis-SerLeuTr 540
Db      1879 GGGAAATGTTACTTGGCAGAAAT---GGTTTCCATTTTGGACATTAATTCACCTTAATAGCAG 1937
Qy      540 pMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLe 560
Db      1938 CTGTCTCCGGTACACCTGTGGGTCACTGTGGAAGCCACCGAGGCTGTATGAAGCACT 1997
Qy      560 uLeu-----GlyCybProValProLeuGlyValLysGlnLysLeuLeuHis 575
Db      1998 CGCAGCAGTGTATCAACACGGCTGCTCTCGGACTTTCATGCGCCAGAGGCGCTTC-- 2055
Qy      575 sTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAl 595
Db      2056 -TGAGACAGAGATCTTTGGAAAGTGAAGAAACACACAGTCAAGACAAATTTCTGAAGC 2114
Qy      595 asPheHisCybLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPh 615
Db      2115 CATAAACATC-----AATTCCTTGTGTGAAGTGTGGCTCATTTATTA 2156
Qy      615 eGlnGlu-ValTrp-----LeuProIleAsnGlnLeuAspLeuLeuAlaSerSerP 633
Db      2157 TCAAGAGATGATCATCCAAATCAAGCTCTGAGCCAGCAAGATTTGAAGCTT-----TCTT 2207
Qy      633 heCybLeuGlnHisCybProTyrLeuArgLysIleArgValAspValLysGlyIlePheP 653
Db      2208 TCAAGGTA-----AAAGCTTATATATGCAATCTCAGAGAAATCC 2246
Qy      653 roArgAsp-----GluSerAlaGluAlaCybProValVal----- 664
Db      2247 CGATTACTATTTGACTTCTTTGAACATTTGGCCAAATTTGCAAGTCCCTGGAATTCAT 2306
Qy      665 -----ProLeuTrpMetArgAspLysThrLeuIleGluGln- 677
Db      2307 TAAACTGACTTTTATGGGAGACTATGGCTTCAATGGAAAGGCTGCAGAAAGCACAGG 2366
Qy      678 TrpGluAspPheCybSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly 697
Db      2367 TGG-----AATCCACAT----- 2378
Qy      698 SerSerIleLeuThrGluArgAlaMetLysThrLeuCybAlaLysLeuAspArgHisProThr 717
Db      2379 -----GGAAAGAGGCCCAAGAACTTACATTCGCCAG----- 2408
Qy      718 CybLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeu 737
Db      2409 ---CAGGCGTATCTTT---GTTCTTCACTGGAAAGCAGAAATTCAGAG-CTC 2455
Qy      738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeu 757
Db      2456 TGGAGGTC-AACATC-----CGGAAATTCAGAAATTCGAT----- 2490
Qy      758 LysGluGluAspValArgMetAlaCybGluAlaLeuLysHisProLysCybLeuLeuGlu 777
Db      2491 ---AAGCAAGATATCAGATATCTGGGAAATATTCAGCTCT-----GCCACA 2535
Qy      778 SerLeuArgLeuAsp-----CysCybGlyLeuThrHisHisAlaCybTyrLeuLysIle 794
Db      2536 AGCTTACGGCTCGAAATTAAGATGTCGTGTGTGCTGGAAAGC-----CTC 2583

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Oy	795	serGlnIleuThrPheProSerLeuysSerLeuSerLeuIaGlyAsnIleVal	814
Db	2584	AGTTGGTCTCCAGACCTGTAAGAACATTATTTCTCATGTGGGAAGCAGTCCCTC	2643
Oy	815	ThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysVala--Leu	833
Db	2644	ACC-----ATGAGAGATGAGAGGACATCATCATCTGTGAACAACTGT	2685
Oy	834	GlnIleuLeuIleLeuGluAspCys-----GlyIleThrAlaThr	846
Db	2686	AAACCTTGAGTATTCATGACCTTACAGAAATCAACGCTCCGGGTGTCTGACT---	2739
Oy	847	GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrIhIleCysIleu	866
Db	2740	-----GACAGCTGGGTACTTGAAGAACCTTACAAAGCTCATATG	2781
Oy	867	SerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuPro	886
Db	2782	GATAAACATTAAGAGATGAAGAAGAGCTATTAACTAGCTGAAGCCTGAAG---	2835
Oy	887	HisCysSerLeuGlnArgMetLeuAsnGlnCysHisIleuAspThrIlaGlyCysGly	906
Db	2836	-----AACCTGAAGAGATGTGTTATTTTCAT-----	2862
Oy	907	PheLeuAlaLeuAlaLeuMetGlyAsnSerTripleThrHisIleuSerLeuSerMetAsn	926
Db	2863	-----TTGACCCCACTGTCT-----	2877
Oy	927	ProValGluAsp-----AsnGlyValIleuLeuLeuCysGluValMetArgGluProSer	944
Db	2878	-----GACATTGAGAGAGGAATGATTACATTAAGCTCTGTCAAGTGAACCC	2928
Oy	945	CysHisIleuGlnAspLeuGlnLeuValIleCysHisIleuThrAlaAlaCysCysGluSer	964
Db	2929	TGTGACCTTGAAGAAATTCATTATGTGTCCTCGCTGGCTTGTCGAATAAGCAGTAATC	2988
Oy	965	LeuSerCysValIleSerArgSerArgHisIleuIleuSerLeuAspLeuThrAspAsnAla	984
Db	2989	CTAGCTCGAAATCTTCCCAATTTGGTCAACCTGACGATCTCTGTGATTAATCGAAATATAC	3048
Oy	985	LeuGlyAspGlyValAlaAlaLeuCysGlnGlyLeuIleuIleuValAsnSerVal---	1003
Db	3049	CTGGAAGAAAGATGAAGATGAAGCTCTTCATGAACATGATCGACAGATGAACGTCTAGA	3108
Oy	1003	-----	1003
Db	3109	CAGTCACCGCAGTCGATGTCGCTGGGGCTGTGTAGCTGCAAGGACAGCCTGACGACCTG	3168
Oy	1004	-----LeuThrArgLeuGlyIleuValAlaCysGlyLeu	1014
Db	3169	TTGAAACATTTGGAGAGAGCTCCCAACATCTGTCAGAGCTGTGGATGAAGAACTGAGACTC	3228
Oy	1015	ThrSerAspCysCysGluAlaIleuSerLeuAlaLeuSerCysAsn-----ArgHisIleu	1032
Db	3229	ACAGATACAGAGATTAGAAATTTTAGTGTCATTTTGTGAAGAAGAACCTGTGAAGAACTTC	3288
Oy	1033	ThrSerLeuAsnLeuValGlnAsnAsnPheSerProIleuGlyMetMetIleuCysSer	1052
Db	3289	CAGCAGTTGAATTTGGCCGGAATCTGTGTGACAGCTGATGATGGCTTGCTCATGGCT	3348
Oy	1053	AlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuThrPlySerGlnIleu---	1071
Db	3349	GTAATTT-----GAGAAATTTTAAGCAATTAGTGTTTTGTGACTTTAGTACTAA	3396
Oy	1072	-----ProValGlnIleArgIleuIleu-----	1078
Db	3397	GAAATTTCTACCTGATCCAGCATTAAGTACAGAAACTTATACCAAGTGTATCCAACTTAAT	3456
Oy	1079	---LeuGlnGluValGlnIleuLeuIleuValProArgValAlaIleAspGlySerTripleHisSer	1097
Db	3457	TTTCTGCAGAGAGCTAAGCTGTGT-----GGGTGG---CAA	3489

RESULT 13
 US-11-145-631-12/c
 ; Sequence 12, Application US/11145631
 ; Publication No. US20060003409A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Betting, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
 ; FILE REFERENCE: 07334-329001
 ; CURRENT APPLICATION NUMBER: US/11/145,631
 ; CURRENT FILING DATE: 2005-06-06
 ; PRIOR APPLICATION NUMBER: US/09/841,739
 ; PRIOR FILING DATE: 2001-08-29
 ; PRIOR APPLICATION NUMBER: US 09/697,089
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: US 60/161,822
 ; PRIOR FILING DATE: 1999-10-27
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 3615
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-145-631-12

Alignment Scores:
 Pred. No.: 1,91e-14 Length: 3615
 Score: 276.00 Matches: 254
 Percent Similarity: 37.03% Conservative: 193
 Best Local Similarity: 21.04% Mismatches: 423
 Query Match: 3.90% Indels: 340
 DB: 8 Gaps: 56

US-10-066-521-6 (1-1344) x US-11-145-631-12 (1-3615)
 QY 17 CysLeuTyrgLueuAeApLygIuGluPhgElnThrPheLygSGLueuLySlyVlyS 36
 Db 3075 TGCtGGCGAGAAAGGTGAGGAGAGATGCTGCTAGAGGGATCATTCATGATTTGAAAAG 3016
 QY 37 SerSerGluSerThrThrCysSerTleProGlnPheGluIleGluAlaSerValGlu 56
 Db 3015 GGTTCAAGATCC-----TGTAACCTC----- 2995
 QY 57 CysLeuAlaLeuLeuLeuHisGluTyrrTyGlyAlaSerLeuAlaTPrAlaThrSerIle 76
 Db 2994 -----TTCTTAATACCTTTAAGAGTGG-----AACTAT 2965
 QY 77 SerIlePheGluAenMetAenLeuArgThrLeuSerGluTySAlaArgAspMetLyS 96
 Db 2964 CCTGATTTCAGAGCTTGATGACAAAGTTTGAGAGACACAGATTTGGCTTCTT 2905
 QY 97 LysIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlu 116
 Db 2904 AACATCACCTCTCTCAATAGGCTTTTTCATGACATCAGACAGAGAGACTTGGACAT 2845
 QY 117 IleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHis 136
 Db 2844 TTGGCTCAGAGTTTAAAGAACTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTT 2785
 QY 137 GlyGlyAspThrTrpAspTyrrLySerSerHisValMetThrTySPhaIaGluGluGluAsp 156
 Db 2784 GGTGAAGATATT---GACATTTATTTTAACTTGAAAAGACACTTCACAGAACTGTCTG 2728
 QY 157 ValArgTrSerSerPheGluAenThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGly 176
 Db 2727 TGGAGAAAGACCAACCATCACCGGTGGAGAGACTGACCCCTGAATGGCTCTGACAG 2668
 QY 177 AlaPheAspSerAspAlaGlyTrpGlyPheArgProArgThrValValLeuHisGlyLySer 196
 Db 2667 GCTCTTCAGACC-----CCCTGCATCATGAAAGGGAAATCT 2632

Oy	197	GLYTLLEGLYSESERALEVALARGRGLLEVALLEUCYSTPRALAGINGLYGLYLEU	216
Db	2631	GGCAAGGCGAAGTCCACTCTGCTCAGAGGAATTCCTCTGGGGCTCCGAAAGTCC	2572
Oy	217	TYRGLN---GLYMETPHESETYRVALPHEPHEUPROVALAGLUMETGLNARGLYS	235
Db	2571	AAGGCTGACCAATTCATATGCTGTCTCTCTCCGTCCAGACGGCCAG-----	2518
Oy	236	LYSGLUSERSERVALTHRGHPHEILESERARGLUTRPROAP-----	250
Db	2517	-----GGTGACCTTTTGGAAACCTCTGATGATCAACTCTGGATATPACTGACATC	2464
Oy	251	---SERGINALPROVALTHRGHILEMETERARGPROGINARGLEUPHEILE	269
Db	2463	AGGAAGCAGACATTCATGCGCATGCTGGAAGTCCGGCAGAGGGTCTTTCTCTT	2404
Oy	270	ASPGLYPHEAPRPLEUGLYSERVALLEUAMNHNPTRHLYSLEYASRPLTR	289
Db	2403	GATGGCTACATGATTC-----AAGCCCAAGACTGCCAGAA-----	2365
Oy	290	ALAGLUYSGINPROPHETHPHELEUILEARSERLEUENARGLYSVALLEUCLEUPRO	309
Db	2364	-----ATCGAACCCCTGATTAAGAAACCAACCGCTTC	2332
Oy	310	GLUSERPHELEULEVALTHR-----VALARGPVALGLY	321
Db	2331	AAGAACATGTCATCTGTCCACCACTACCACTAGTCCCTGAGGACATPACGSCAATTTGGT	2272
Oy	322	THRGHUYLEUYSERGLYVALVALSERPROARGTYLEULEUVALARGGLYLESER	341
Db	2271	GCC-----CTGACCTGTGAGGTGGGATATGACAGAAAGCAGCGCCAGGCTCTCAT	2218
Oy	342	GLYGLUGINARGILEHLEULEUENLEUGLNYARGLYLEGLYHNSGLNYSTHGLN	361
Db	2217	CGAGAGTGCATATAGAGAGCTTCTGAAAGCTTGTCTCCAAATTCAGAAATTCAGG	2158
Oy	362	GLYLEUARGALILEMETASNHARGGLYLEUENBERGLNYSGINLPROALVAL	381
Db	2157	TGCTTGAAGGATCTCATG-----AAGACCCCTCTCTTT	2125
Oy	382	GLYSERLEULEYCVALLALEUGLNUENGINBRVALVALGLYGLUSERVALALAPRO	401
Db	2124	GTGCTCATCACTGTG---GCAATCCAGTGG-----GGGAAAGGAGTTCAC	2080
Oy	402	PHEANGLNTHRLEUTHRGLYLEUHSIALAPHEVALPHEHISGLNLEUTHRPROARG	421
Db	2079	TCTACACACAAACAAAGCTGTTCAT-----ACCTTCATGATCTG-----	2038
Oy	422	GLYVALVALARGARGCYALEUENLEUGLNUARGVALVALLEUYSARGPHECYARG	441
Db	2037	---TTGATACAGAAAAACAAACACAAACATTAAGGTGTGGCTGCAAGTCACTTATTCGG	1981
Oy	442	-----METALVALGINLYVALITPRANARGLYSERVALPHE	454
Db	1980	AGCCTGGACCACTGGAGACCTACTCTGGAGGGGTGTCTCCACAAAGTTGATTC	1921
Oy	455	ASPGLYASPRPLEUMETVALGINGLYLEUGLYGLUSERGLYLEUARGALALEUPHEHIS	474
Db	1920	GAACTGCAGAGAT-----GTGCCAGCGTGAATGAG-----	1891
Oy	475	METANILILEULEUPROAPSERHISCYSGINLUITYR-----	487
Db	1890	---GATGCTCTGCTCAACATGGGGCTCTCTGTAATATPACAGCTCAAAAGTTCAAGCCA	1834
Oy	488	---TYRTHRPHENHISLEUSERLEUGLNUBRPHECYVALALALA-----LEUITYRYX	504
Db	1883	AAGTATAATTTCTTCCACAGTCATTCACAGAGGTACACAGACGACGAAAGTCAAGAGT	1774
Oy	505	VALLEUGLUGLYLEUGLNULEGLUPROALALEUCYSPROLEUTYRVALGLUYSTHRYLS	524
Db	1773	TTATTGACGTCTCATGAGCCAGG-----GAGGTGACCAAG	1738

QY	525	ArgSerMetGluLeuLysGlnAlaGlyPheHis-----IleHis-SerLeuThr	540
Db	1737	GGGATATGCTTTCGCAAAAAT--GGTTTCATTTTCGACATTAATCATCCACTTATATGACG	1675
QY	540	pMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValIle	560
Db	1678	CCTGCTCCGGTACACCTGTGGTCTACTCTGTGGAAAGCCACCGAGGCTGTATATACACACTT	1611
QY	560	uLeu-----GlyCysProValProLeuGlyValLysGlnLysLeuHis	575
Db	1618	CGACGACAGTATATCAACAGGGGTGGCTCTCGGAACTTTTCATTCGCCAAGAGGCTCTC--	1561
QY	575	sTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAl	595
Db	1560	-TGGAGACAGAAATCTTTGGCAAAAGTGTGMAAAACACACCTGACGACAAATTTCTAAAGC	1503
QY	595	aPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPh	615
Db	1501	CATTAACAATC-----AATTCTTTGTAGAGTGTGGCATCATTTATAT	1463
QY	615	eGlnGlu-ValTrp-----LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerP	633
Db	1459	TCAATAGAGTACATCCAAATACAGCCCTGACGCAAGAAATTTGAAGCTT-----TCTT	1400
QY	633	heCysLeuGlnHisCysProGlyLeuArgLysIleArgValAspValLysGlyIlePheP	653
Db	1408	TCAAGGTA-----AAAGCTTATATATCAACTACAGGGAATATCC	1370
QY	653	roArgAsp-----GluSerAlaGluAlaCysProValVal-----	664
Db	1369	CGATTACTTATTTGACTCTTTTGAACATTTTGCCCAATGTGTCAAGTCCCGCTGACTTCAT	1311
QY	665	-----ProLeuThrPheArgAspLysThrLeuLeuLeuGlnGln-	677
Db	1309	TAAATCGACTTTTATGGGGGAGCGTATGGCTTCATGGGAAAAGCTGCAGAAACACAGG	1255
QY	678	TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly	697
Db	1249	TGG-----AATCCACAT-----	1238
QY	698	SerSerIleLeuThrGluArgAlaMetLysThrLeuCysValaLysLeuArgHisProThr	717
Db	1237	-----GAAAGAGGCCCCGAAACCTTACATTTCCAG--	1200
QY	718	CysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeu	737
Db	1207	-----CAGGCGCTGATCTTT--GTTCTTCAACTGGAAGCAGGAATTCAGGA-CTC	1165
QY	738	TrpArgIleValaMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeu	757
Db	1160	TGGAGGTC-ACACTC-----CGGGATTTACAGCAAGTTGAAT-----	1128
QY	758	LysGlnGluAspValArgMetAlaCysGlnAlaLeuLysHisLeuProLysCysLeuLeuGlu	777
Db	1135	--AAGCAAGATATAGATATCTGGGAAAATATTCAGCTT-----GCCACA	1081
QY	778	SerLeuArgLeuAsp-----CysCysGlyLeuThrHisAlaCysGlyThrLeuLysIle	794
Db	1080	AGCCTCAGGCTCAAAATAAGAGATGTGCTGTGTGGCTGGAGAC-----CTC	1033
QY	795	SerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysVal	814
Db	1032	AGTTTGGTCTCAGCAGCTGTATGAACAATTTATCTTCATGATGATGAGACAGTCCCTTC	973
QY	815	ThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAla---Leu	833
Db	972	ACC-----ATMAAAGATGAGAGCAGCATCATCTGTAACAAACTTG	931
QY	834	GlnLysLeuIleLeuGluAspCys-----GlyIleThrAlaThr	846
Db	930	AAACACTTGAGTATTCATGACTTACAGAAATCAACAGGCTCCGGGTGTGTGACT-----	877
QY	847	GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu	866

US-11-128-061-3918
Sequence 3918, Application US/11128061
Publication No. US20060003958A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3918
LENGTH: 536
TYPE: DNA
ORGANISM: Cricetus griseus
FEATURE:
NAME/KEY: misc feature
LOCATION: (363)..(379)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-3918

Alignment Scores:

Pred. No.:	3,08e-15	Length:	536
Score:	270.00	Matches:	64
Percent Similarity:	50.00%	Conservative:	30
Best Local Similarity:	34.04%	Mismatches:	66
Query Match:	3.82%	Indels:	28
DB:	8	Gaps:	4

US-10-066-521-6 (1-1344) x US-11-128-061-3918 (1-536)

QY 779 leuArgleuAProSerCySglleuThrAlaCyefyleuSileSerGlnlleu 798
Db 45 CTGAGATTACCTGT-----
QY 799 ThrThrSerProSerleuSleuSerleuAlaGlyAenlyeValThrAsp----- 816
Db 60 -----GCACCCACCATG---AGTCTTGACATCCATGTCAGCTGATGCCAGG 110
QY 817 ---GlnGlyValMetProLeuSerAspAlaleuArgValSerGlnCyAlaleuGlnlys 835
Db 111 TGAGACAGAGCTCTTCCCTGATCCAGCAATACCAAGTGTCCAG----- 155
QY 836 leuIleleuGluAProCySglyleThrAlaThrGlyCySglSerleuAlaSerAlaleu 855
Db 156 -----TTGATGACCTGTGTCTCAGTGGGTGGCGCAAGACATCAGCTCAKCCATT 209
QY 856 ValSerSerAArgSerleuThrAlaCySglleuSerAenSerleuGlyAenGlnGly 875
Db 210 CAGTCCAAACCCCTTAACAGAGCTGATGACCAATGAGCTGGGGACCTGGC 269
QY 876 ValAsnleuLeuCySArgSerMetArgleuProHisCySleuSerleuGlnArgleuMetleu 895
Db 270 GTGTGCTGTGATCCACAGGCTGACAGATCCACCTTAAGATCCAGAGCTAAGCTG 329
QY 896 AsnGlnCySHisleuAProThrAlaGlyCySgllyPheleuAlaleuMetGlyAsn 915
Db 330 CAGATTGACAGCTTGACAGAGCTGCTGTAGANNNNNNNNNNNNNNNAAGTCTTTA 389
QY 916 SerTrpleuThrHisleuSerleuSerMetAsnProValGluAProAsnGlyVallyleu 935
Db 390 CTAACCTGGGGAGGATACATCTCAGTGTATATCTCTGGGAGATGACAGTCTGAAGCTG 449

QY 936 leuCySgllyValMetArgGluProSerCySHisleuGlnAProleuGluVallySlysCyS 955
Db 450 CTCTGTGAAGAGACTTCTGACACCCCAATGCGGCTTGAGAAAGCTTCAGTTGAAATCTGT 509
QY 956 HisleuThrAlaAlaCySglly 963
Db 510 AACCTCAAGCTTACCAAGTTGCCAG 533

Search completed: January 21, 2006, 13:04:31
Job time : 531 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 21, 2006, 05:50:17 ; Search time 2275 Seconds

(without alignment)
4885,294 Million cell updates/sec

Title: US-10-066-521-6

Perfect score: 7074
Sequence: 1 MEGXSLTSPSYGLQWCLYE.....DDHSGVMSLGAAGLEGLVS 1344

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Dgapop 6.0 , Dgapext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US10066521/runat_20012006_145900_21102/app_query.fasta.1.1543
-DB=Published Applications NA Main -QFMT=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPRMT=pct -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10066521@cgn_1_1_1594@runat_20012006_145900_21102 -NCPU=6 -ICPU=3
-NO MAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=10 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELXT=7

Database : Published Applications NA Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7074	100.0	4035	5	US-10-124-498-5
2	7074	100.0	4035	5	US-10-066-521-5
3	5756	81.4	3489	7	US-10-416-642-3
4	5756	81.4	3926	6	US-10-216-645-1
5	5741.5	81.2	3885	8	US-10-860-761-3
6	5741.5	81.2	3900	7	US-10-399-443-23
7	5741.5	81.2	3900	7	US-10-677-943-23

8	5683.5	80.3	3830	6	US-10-216-645-3	Sequence 3, Appli
9	5120	72.4	3226	7	US-10-092-900A-347	Sequence 347, App
10	2688	38.0	3447	7	US-10-399-443-5	Sequence 5, Appli
11	2688	38.0	3447	7	US-10-677-943-5	Sequence 5, Appli
12	2005	28.3	1157	7	US-10-399-443-1	Sequence 1, Appli
13	2005	28.3	1157	7	US-10-677-943-1	Sequence 1, Appli
14	1885.5	26.7	3521	8	US-10-794-342-2	Sequence 2, Appli
15	1435	20.3	3368	5	US-10-124-498-23	Sequence 23, Appli
16	1435	20.3	3368	5	US-10-066-521-23	Sequence 25, Appli
17	1434	20.3	2982	5	US-10-124-498-25	Sequence 25, Appli
18	1434	20.3	2982	5	US-10-066-521-25	Sequence 25, Appli
19	1434	20.3	2985	6	US-09-965-621-15	Sequence 15, Appli
20	1434	20.3	2985	6	US-10-407-866-15	Sequence 15, Appli
21	1434	20.3	2985	6	US-10-781-294-15	Sequence 15, Appli
22	1402	19.8	2775	7	US-10-357-820-51	Sequence 51, Appli
23	1335	18.9	1075	7	US-10-399-443-3	Sequence 3, Appli
24	1335	18.9	1075	7	US-10-677-943-3	Sequence 3, Appli
25	1332.5	18.8	3484	8	US-10-794-342-3	Sequence 3, Appli
26	1320.5	18.7	3108	3	US-09-965-621-23	Sequence 23, Appli
27	1320.5	18.7	3108	6	US-10-407-866-23	Sequence 23, Appli
28	1320.5	18.7	3108	7	US-10-781-294-23	Sequence 23, Appli
29	1315.5	18.6	3190	6	US-10-094-749-1079	Sequence 1079, Ap
30	1315.5	18.6	3172	7	US-10-399-037-74	Sequence 74, Appli
31	1314.5	18.6	2883	7	US-10-161-432-3	Sequence 3, Appli
32	1313.5	18.6	3540	8	US-10-794-342-7	Sequence 7, Appli
33	1304.5	18.4	3218	6	US-10-407-866-67	Sequence 67, Appli
34	1303.5	18.4	3186	5	US-10-124-498-17	Sequence 17, Appli
35	1303.5	18.4	3186	5	US-10-066-521-17	Sequence 17, Appli
36	1289.5	18.2	2575	3	US-09-848-035-7	Sequence 7, Appli
37	1289.5	18.2	2575	3	US-09-986-224-7	Sequence 7, Appli
38	1289.5	18.2	2575	9	US-10-116-422-7	Sequence 9, Appli
39	1255	17.7	3102	5	US-10-127-516-6	Sequence 6, Appli
40	1255	17.7	3102	6	US-10-027-629-6	Sequence 6, Appli
41	1255	17.7	3102	6	US-10-132-967-6	Sequence 6, Appli
42	1255	17.7	3857	5	US-10-127-516-4	Sequence 4, Appli
43	1255	17.7	3857	5	US-10-027-629-4	Sequence 4, Appli
44	1255	17.7	3857	6	US-10-132-967-4	Sequence 4, Appli
45	1250.5	17.7	3531	9	US-10-756-149-3252	Sequence 3252, Ap

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
; US-10-124-498-5

Alignment Scores:

Pred. No.: 0 Length: 4035
 Score: 7074.00 Matches: 1344
 Percent Similarity: 100.00% Conservat: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

QY 1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTyrCysLeuTyrGlu 20
 DB 1 ATGAGAAAGAGCAAAATGCTCACTTTTCCAGCTACGAGCTGCAATGCTCTTAAGAG 60
 QY 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysSerSerGlnSer 40
 DB 61 CTAGACAGAGAAAGATTTCAGACATTCAAGAAATTACTAAAGAAAGAAATCTTCGAATCG 120
 QY 41 ThrThrCysSerLysProGlnPheGlnIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
 DB 121 ACCACATGCTCTATTCACAGTTTGAATCGAAGATCCCAACGTGGAATGCTGGCACTC 180
 QY 61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaThrIleThrSerLysSerLysPheGlu 80
 DB 181 CTCTTGATAGATATTAATGAGACATGCTGAGCTGAGCTCATTCATTCATTCGATGAA 240
 QY 81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysLysSerGln 100
 DB 241 AACATGAACCTGCGAACCTCTCGAGAAAGCAAGGATGACATGAAAGAAATTTTCACAA 300
 QY 101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGluLysSerGlnAla 120
 DB 301 GCTATGAAACAAAGAAAGTGCACAGCAGCAGAGACAAAGAAATTTTCACAAAGCT 360
 QY 121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGluLysGlyLysAspThr 140
 DB 361 ATGGAACAAAGAGTGCACAGCAGCAGAGACAAAGAAATGAGAGTGAACA 420
 QY 141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
 DB 421 TGGGACATCAAGAGTCACTGATGACCAATTCGCTGAGAGAGATGATACGTCTGATG 480
 QY 161 PheGluAsnThrAlaAlaAspTyrProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
 DB 481 TTTGAAACAACTGCTGCTGACCTGGCCGAAATGCAAACTGCTGCTTTTGAATTC 540
 QY 181 AspArgTrpGlyPheArgProArgTrpValValLeuHisGlyLysSerGlyLysGlyLys 200
 DB 541 GACCGAGTGGGCTTCCGAGCTCGACAGTGTCTGACGGAAGTCAAGAAATGGAGAA 600
 QY 201 SerAlaLeuAlaArgArgLysValLeuLysCysTrpAlaGlnGlyLysLeuTyrGlnGlyMet 220
 DB 601 TCGGCTCTTACCGAAGAGATGCTGTCTGCTGGGCGCAAGTGGACCTCTACCGAGATG 660
 QY 221 PheSerTyrValPhePheLeuProValArgLysMetGlnArgLysLysSerVal 240
 DB 661 TTTCTCCATCACTCTTCTCTCCCGTTAAGAGATGACGCGGAAGAGAGAGAGAGTGC 720
 QY 241 ThrGluPheLysSerArgGluTyrProAspSerGlnAlaProValThrGluLysMetSer 260
 DB 721 ACGAGATTCATCTCCAGAGAGTGCAGACCTCCAGAGCTCGGAGAGAGAGATATGCTC 780
 QY 261 ArgProGluArgLeuLeuPheLysLysAspGlyPheAspAspLeuGlySerValLeuAsn 280
 DB 781 GAGACAAAGAGGCTGTTGTTTCATTCATTCAGCGTTTCATTCAGCTGCTGCTCTCAC 840
 QY 281 AsnAspThrLysLeuLysLysAspTyrAlaGluLysGlnProPheThrLeuLysArg 300
 DB 841 AATGACCAAAAGCTCTGCAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuLysValThrValArgAspVal 320
 DB 901 AGTCTGCTGAGAGAGAGTCTGCTCTGAGTCTTCTGATGATCACTGATCAAGAGAGT 960

QY 321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGlyTyr 340
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 QY 341 SerGlyGluGlnArgLysLysLeuLeuLeuGluGlnArgGlyLysGlyGluHisGlnLysThr 360
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 QY 361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
 DB 1081 CAGAGGTGCTGCTGATCAAGAACACCGTAGACTGCTCAACAGTCCAGAGTCCCGGCC 1140
 QY 381 ValGlySerLeuLysCysValAlaLeuGlnLeuGlnAspValValGlyLysSerValAla 400
 DB 1141 GTGGGCTCTCTCATCTGCTGAGCTGAGCTGAGCTGAGAGAGAGAGAGAGAGAGAG 1200
 QY 401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
 DB 1201 CCTTCAACCAACAGCTCAAGAGCTGACAGCGCTTTGTGTTCATTCAGCTCACCCCT 1260
 QY 421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCys 440
 DB 1261 CAGAGCTGCTGCTCGGCGCTGCTCTCATCTGAGAGAAAGATTCCTGGAAGCTTCTGC 1320
 QY 441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
 DB 1321 CGTATGCTGAGAGAGAGTGTGAATAGGAATGATGTTGATGTGATGATGATGATGAT 1380
 QY 461 ValGlnGlyLeuGlyLysSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuPro 480
 DB 1381 GTTCAGAGAGCTCGGAGAGTGTGAGCTCGTGTCTGTTCATGAAACATCTCTTCCA 1440
 QY 481 AspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
 DB 1441 GACAGCCACTGTGAGAGATCTACACTTCTTCCACTGACTCTCCAGACTTCTGTGCC 1500
 QY 501 AlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrVal 520
 DB 1501 GCCTTGATCACTGATGAGAGAGCTGGAATGAGCACTCTGCTCTGCTGATGATG 1560
 QY 521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisLysLysSerLeuTyr 540
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 DB 1621 ATGAAAGCTTCTTGTGTGCTCTGATGAGGAAGATGAGAGAGCCACTGAGAGTCTG 1680
 QY 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
 DB 1681 CTGGGCTGTCCCTTCCCTGGGAGTGAACAGAGCTTCTGCACTGGGCTCTCTGTTG 1740
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 DB 1741 GGTCAAGAGCTTATGCAACACCCAGAGACACCTGAGAGCTTCCACTGCTTTC 1800
 QY 601 GlnThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
 DB 1801 GAGACTCAAGCAAAAGATTTGCTGCTTGGCTTAACAGCTTCCAGAAAGTGTGCTT 1860
 QY 621 ProLysAsnGlnAsnLeuAspLeuLysLysSerPheCysLeuGlnHisCysProTyr 640
 DB 1861 CCGATTAAACAGAACTGAGATTCATTCCTTCTGCTCCAGCACTGCTCCCTAT 1920
 QY 641 LeuArgLysLysArgValAspValLysGlyLysPheProArgAspGlyLysAlaGluAla 660
 DB 1921 TTGGGAAATTCGGAGAGTGTCAAGAGAGATCTTCCAGAGATGATGCTGAGAGCA 1980
 QY 661 CysProValValProLeuTyrMetArgAspLysThrLeuLysGluGlnTyrGluAsp 680
 DB 1981 TGTCTGTGCTCTCTATGATGAGAGTGGAGATTAAGACCTCATTTAGAGAGAGTGGAGAT 2040
 QY 681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700


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Db      2041 TTCTGCTCCATGCTTGGACCAACCACTGGCGGAGCTGGACCTGGGAGGAGCATC 2100
Qy      701  LeuThrGluArgAlaMetIleYThrLeuCyAlaIleuArgH1SerProThyValIle 720
Db      2101 CTGACAGAGGGGGGCAAGAAACCTGTGTGCGAAGCTGAGGCAATCCCACTGGCAAGATA 2160
Qy      721  GluThrLeuMetPheArgAspAlaGlnIleThrProGlyValGlnH1SleuTriArgIle 740
Db      2161 CAGACCTGATGTTTAAAGATGACAGATTACCCCTGGTGTGACAGCACTCTGGAGAAATC 2220
Qy      741  ValMetAlaAsnArgAsnLeuArgSerIleuAsnLeuGlyIleThrH1SleuLeuGlyIle 760
Db      2221 GTCATGGCCCAACCGTAACCTTAAGATCCCTCAACTGGGAGGCAACCACTGAAGAAAGAG 2280
Qy      761  AspValAlaArgMetAlaCyArgIleAlaLeuIleH1SerProIleYThrLeuLeuSerIleuArg 780
Db      2281 GATGTAAAGATGGGGGTGAAGCCTTAAACCAACCAAAATGTTGTGAAGTCTTTGAAGG 2340
Qy      781  LeuAspCyArgGlyLeuThrH1AlaCySerIleuIleSerGlnIleLeuThrThr 800
Db      2341 CTGATTTGCTGTGATGATGACCAATGCTGTTAACCTGAAGATCTCCCAATCTTTACCAAC 2400
Qy      801  SerProSerLeuIleYSerLeuSerIleuAlaGlyAsnIleValIleAspGlnIleValMet 820
Db      2401 TCCCCAGCGCTGAATCTCTGAGCCTGGCAGAAACAAAGTGACAGACCAAGAGTAATG 2460
Qy      821  ProLeuSerAspAlaLeuArgValIleSerGlnIleAlaLeuGlnIleValIleLeuGluAsp 840
Db      2461 CCTCTCAGTATGCTTGAAGAGTCTCCAGTGGCCCTGCAAGAGCTGATATCTGAGAGAC 2520
Qy      841  CyArgIleIleThrAlaThrGlyCyArgIleSerIleuAlaSerAlaLeuValIleAspArgSer 860
Db      2521 TGTGGATTCACAGCCACGAGGTTGCCAAGTCTGGCCTCAGCCCTGTGACAGAACCGAGAC 2580
Qy      861  LeuThrH1SleuCyAlaSerAsnAsnSerLeuGlyIleAsnGlyIleValIleAsnLeuIleCy 880
Db      2581 TTGACACACCTGTGCTATTCACACACAGCTGGGGAACGAAGGTGAATCTACTGTGT 2640
Qy      881  ArgSerMetArgLeuProH1SleuSerIleuGlnArgMetLeuAsnGlnCyH1Sleu 900
Db      2641 CGATCCATGAGGCTTCCCATGTAGTCTGCAAGGCTGATGCTGAATCACTGACCACTG 2700
Qy      901  AspThrAlaGlyCyArgIlePheLeuAlaLeuAlaLeuMetGlyIleAsnSerTriLeuThrH1S 920
Db      2701 GACACGGCTGAGCTGTGTTTCTTGCACTTGCCTTATGGTAACTCATGCTGAAGAC 2760
Qy      921  LeuSerLeuSerMetAsnProValGluAspAsnGlyIleValIleLeuLeuCyArgIleValMet 940
Db      2761 CTGAGCCTTAGCAAGAACCTGTGGAAGACAAATGGCGTGAAGCTTCTGTGGAGGTATG 2820
Qy      941  ArgGluProSerCyH1SleuGlnAspLeuGluValIleYCyH1SleuThrAlaAla 960
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Qy      961  CyArgGlyIleSerLeuSerCyValIleSerArgSerArgH1SleuYSerIleuAspLeu 980
Db      2881 TGCCTGTGAAGTCTGTCTGTGTGATCTCGAGAGCAACACCTGAGAGAGCTGATCTTC 2940
Qy      981  ThrAspAsnAlaLeuGlyAspGlyIleValIleAlaLeuCyArgIleValIleGlyIle 1000
Db      2941 ACGGACAAATGCGCTGGGAGCGGTGGGTCTGTGGCTGCGAGGAGCTGAAGCAAAAG 3000
Qy      1001  AsnSerValIleuThrArgLeuGlyIleuValAlaCyArgIleLeuThrSerAspCyArgIle 1020
Db      3001 AACAGTGTCTGACGAGACTCGGGTGAAGCACTGTGACCTGACCTTGATTTGCTGTAG 3060
Qy      1021  AlaLeuSerLeuAlaLeuSerCyAsnAspArgH1SleuThrSerLeuAsnLeuValGlnAsn 1040
Db      3061 GCACCTTCCTGGCCCTTCTCTGCAACCGGCACTGACCACTTAACCTGTGTGAGAAAT 3120
Qy      1041  AsnPheSerProIleGlyMetMetIleuCySerAlaPheAlaCyProThrSerAsn 1060

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Db      3121 AACTCAGTCCCAAGAAAGATGATGAGCTGTGTTCGGCTTGTGCTCCACTCAAC 3180
Qy      1061  LeuGlnIleIleGlyLeuLeuTriPLeuTriPLeuTriPLeuValGlnIleArgIleLeuLeuGln 1080
Db      3181 TTACAGATTAATTTGGGCTGTGGAAATGGCAGATACCTCTGTGCAAAATAGAAAGCTGTGAG 3240
Qy      1081  GluValGlnLeuLeuYProArgValIleIleAspGlySerTriPLeuIleSerPheAspGln 1100
Db      3241 GAATGCAAGCTACTCAAGCCCGGAGTGTGTAATGACGATAGGTGTGGCAATCTTTGATGAA 3300
Qy      1101  AspAspArgH1SleuIleGlyLeuThrPheArgLeuProGlnIleSerArgAlaTriPProCy 1120
Db      3301 GATGACCGACCAAAATGACCTTAATCTTCCGCTCCCTGAAGACCGGCAATGGCCATGT 3360
Qy      1121  AlaLeuLeuTriPLeuMetAsnProGlnIleIleYSerArgValIleSerLeuAlaGlyAsp 1140
Db      3361 GCTTGTGTTGGGAGATGAACCCAGAGCAAGAAAGCTGTGTGTGCTTCTGTGGAGAC 3420
Qy      1141  PheIleSerSerThrArgPheAlaIleYSerIleuCyAlaLeuAlaThrAlaAsnGlyIleSer 1160
Db      3421 TTCAAGAGCAGTACACAGATTTGCCAAGTCTGTGCTGGCCAGCGCAAAATGTGATGCC 3480
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Db      3601 GGGCTTGATCAACAGTGTGATCATGACCAAGAGGTATGGCTGTGCTGACTGAGGAGA 3660
Qy      1221  GluLeuSerSerArgIleuCyArgProThrValIleuMetThrThrAlaValCyProGly 1240
Db      3661 GAGCTGAGCTCGAGGGCTGTGTCCAAAGTGTGATGACCAAGCGGTGTGTCTGTGT 3720
Qy      1241  HisTriPLeuArgLeuGlyIleSerArgGlyIleTriPLeuAsnSerAlaAspAspH1Sleu 1260
Db      3721 CACTGGAGCGGCTGGGCTTGAAGGGCTGTGTCTTAAGTCTGATGACCAAGCGGT 3780
Qy      1261  ValSerTriPLeuGlyIleAlaGlyIleuGlnIleuValIleSerAsnSerAlaAspAsp 1280
Db      3781 GTGTCTGTGATCAGGAGCGGCTGGGCTGAGGGGCTGTGTGCAACAGCTGATGAC 3840
Qy      1281  HisSerGlyValAlaTriPLeuGlyIleAlaGlyIleuGlnIleuValIleSerAsnSer 1300
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Qy      1301  AlaAspAspH1SleuGlyValIleSerTriPLeuGlnIleAlaGlyIleuGlnIleValIle 1320
Db      3901 GCTATGACCAACAGCGGTGTCTGTGATCTGAGAGCGGCTGGGCTGTGAGGGGCTGTGTG 3960
Qy      1321  SerAsnSerAlaAspAspH1SleuGlyValIleSerTriPLeuGlnIleAlaGlyIleuGln 1340
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Qy      1341  GlyLeuValIleSer 1344
Db      4021 GGGCTGTGTCT 4032

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RESULT 2

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US-10-066-521-5
; Sequence 5, Application US/1006521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001

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QY 601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
 DB 1801 GAGCTCAAGCAAGAGATTGCTTCCTGGCACTTAACACCTTCCAGAGAGTGGCTT 1860
 QY 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640
 DB 1861 CCGATTAAACAGAACTGGAATTGATAGACTTCTTCTGCTCCACAGACTGTCCTGAT 1920
 QY 641 LeuArgLysIleArgValAspValIleGlyIlePheProArgAsnGlnSerAlaGlnAla 660
 DB 1921 TTGGGAAATTCGGGTGATGTCAMAGGATCTTCCAGAGAGTATCCGCTGAGGCA 1980
 QY 661 CysProValValProLeuTrpMetArgAspLysThrLeuIleGlnGluGlnTrpLysAsp 680
 DB 1981 TGTCTGTGTCTCTCTATGAGTGGGATTAAGACCTTCACTTGAAGACAGTGGGAAT 2040
 QY 681 PheCysSerMetLeuGlyThrHisProHisAlaLeuArgGlnLeuAspLeuGlySerSerIle 700
 DB 2041 TTCTGCTCATGCTTGGCACCCACACCTGGCGGAGCTGGACCTGGGAGCAGCATC 2100
 QY 701 LeuThrGluAlaGluAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
 DB 2101 CTGACAGAGCGGCGCATGAGACCTGTGTGCCAAGCTGAGGACATCCACCTGCAGAAATA 2160
 QY 721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIle 740
 DB 2161 CAGACCTGATGTTAGAAATGACACAGATACCTCTGGTGTGACACCTCTGGAGAAATC 2220
 QY 741 ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisAlaLeuLysGlnGlu 760
 DB 2221 GTCACTGGCCAAACCGTAACCTTAAGATCCTCAACTTGGAGGAGCACCTGAGAGAAAG 2280
 QY 761 AspValArgMetAlaCysGlnAlaLeuLysHisProLysCysLeuLeuGlnSerLeuArg 780
 DB 2281 GATGTAAGATGGCGCTGTAAGACCTTAACACCCCAAAATGTTTGTGAGAGCTTTGAGG 2340
 QY 781 LeuAspCysCysGlyLeuThrHisAlaCysThrLeuLysIleSerGlnIleLeuThrThr 800
 DB 2341 CTGATTCCTGGATTAACCAATCCATGCTGTAACTGAAAGATCTCCAAATCTTTACGACC 2400
 QY 801 SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMet 820
 DB 2401 TCCCCACACTGAAATCTCTGAGCCTGGCAGGAAACAAAGTGACAGACCAAGGAGTAATG 2460
 QY 821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840
 DB 2461 CCTCTCACTGATGCTCTGAGAGTCTCCAGTGCCTGCGCAGAACCTGATCTGAGAGAC 2520
 QY 841 CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
 DB 2521 TGTGGCAATCACAGCCAGCGGTGGCCAGAGTCTGCGCTCAGCCCTGTCCAGAACCGGAGC 2580
 QY 861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCys 880
 DB 2581 TTGACACACCTGTGCTATCCAAACACAGCTCGGGGAAAGAAAGTGTAATCTATCTGTGT 2640
 QY 881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
 DB 2641 CGATCAAGAGGCTTCCCACTGTAGTCTGACAGAGGCTGATGCTAACTACAGGCCACCTG 2700
 QY 901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThrHis 920
 DB 2701 GACACGGCTGGGTGGTGTCTTGTGCACTTGGCTTAAGGTAACTCAAGGCTGACGAC 2760
 QY 921 LeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlnValMet 940
 DB 2761 CTGACCTTACGATGAACCTCTGTGAAGACATGGGTGAAGCTTCTGTGGCAGAGTCAATG 2820
 QY 941 ArgGluProSerCysHisAlaLeuGlnAspLeuGlnLeuValLysCysHisAlaLeuThrAla 960
 DB 2821 AGAGAACCACTTGTGATCTCTCAAGAGCTGGAGTGTGTAAGTGTATCTATCAACCGCGCG 2880

QY 961 CysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu 980
 DB 2881 TGTGTGAGAGTCTGTCTGTGTGATCTCGAGGAGACACCTGGAAGAGCTGATCTC 2940
 QY 981 ThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGlnGlyLeuLysGlnLys 1000
 DB 2941 ACGACAAATGCTCGGGTGAAGCGTGGGTTCCTGCTGCTGCGAGGACTAAGCAAAAG 3000
 QY 1001 AsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGln 1020
 DB 3001 AACAGTGTCTGAGAGACTCGGCTTGAAGCACTGGACATGTGACATCTTGAATGCTGTAG 3060
 QY 1021 AlaLeuSerLeuAlaLeuSerCysAsnArgHisAlaLeuThrSerLeuAsnLeuValGlnAsn 1040
 DB 3061 GCACCTCTCTGGCCCTTCTCTGCAACCGGCAATCTGACACAGTCTAAACCTGTGTGAGAT 3120
 QY 1041 AsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060
 DB 3121 AACTTCAGTCTCCAAAGAAATGATGAAGCTGTGTGGCTTGTGCTTCCACAGCTTAAAC 3180
 QY 1061 LeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGln 1080
 DB 3181 TTACAGATTAATGGGCTGTGAAATGGCAATGCACTGTGCAAAATAGAGAACTGTGGAG 3240
 QY 1081 GluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlu 1100
 DB 3241 GAAGTGACGTACTCAAGCCCGGAGTGGTAATGACAGTATGACGATGAGCAATTCCTTGTATGA 3300
 QY 1101 AspAspArgHisLysIleGlyLeuThrPheArgLeuProGlnSerArgAlaTrpProCys 1120
 DB 3301 GATGACCAACAAMATGAGACTTACTTCCGGCTCCCTGAAGCGGCGCAATGCGCATGT 3360
 QY 1121 AlaLeuLeuTrpGlyMetAsnProGlnGlnLysLysArgValSerLeuLeuAlaGlyAsp 1140
 DB 3361 GCTTGTCTGTGGGATTAACCCAGAGCAAGAAAGCTGTGTCTCTCTGCTGGAAC 3420
 QY 1141 PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGlnSer 1160
 DB 3421 TTCAAGACAGATACAGATTTGCCAAGTCTCTGCTCGGCGCAAGCAATGTGTAGTCC 3480
 QY 1161 GlnArgValAspAsnValGlnGlnSerSerProGlnProMetAlaGlyThrGlnHisLys 1180
 DB 3481 CAGAGAGTTGACAAAGTGAGACAGAGCTCCCGCAACCAATGAGCGGACGAGAACAA 3540
 QY 1181 GlnAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGlyLeuGln 1200
 DB 3541 CAAGATTAATGTTGAGTGTGATATTCGGAAGCTGTGTGAACCTGAGCTGACAA 3600
 QY 1201 GlyLeuGlySerAsnSerAlaAspHisAlaAspHisAlaGlyMetAlaTrpSerLeuGlyArg 1220
 DB 3601 GGGCTTGATCAACAGTGGCTGATCATCAACCGAGGATATGGCTGTCACTAAGGAGAA 3660
 QY 1221 GlnLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240
 DB 3661 GAGCTGAGCTGAGGGGCTGTGTGTCCAAAGTGTGATGAACACAGCGGTGTGTCTGTGT 3720
 QY 1241 HisTrpGluArgLeuGlySerArgGlyTyrCysLeuAsnSerAlaAspAspHisSerGly 1260
 DB 3721 CACTGGAGCGGCTGGGCTCTTAAGGGGCTGTGTCTTAACAGTGTGATGAACACAGCGGT 3780
 QY 1261 ValSerTrpSerLeuGlyAlaAlaGlyLeuGlnGlyLeuValSerAsnSerAlaAspAsp 1280
 DB 3781 GTGTCTGTGTCACTGGAGCGGCTGGGCTGAGGGGCTTGTGTCCAAAGTGTGTCTGATGAC 3840
 QY 1281 HisSerGlyValAlaTrpSerLeuGlyAlaAlaGlyLeuGlnGlyLeuValSerAsnSer 1300
 DB 3841 CACAGCGGTGTGTGTGTCTGTGTCACTGGAGCGGCTGGGCTGAGGGGCTTGTGTCCAAAGT 3900
 QY 1301 AlaAspAspHisSerGlyValAspTrpSerLeuGlyAlaAlaGlyLeuGlnGlyLeuVal 1320
 DB 3901 GCTGATGACCAAGCGGTGTGTCTGTGTCACTGGAGCGGCTGGGCTGAGGGGCTTGTGT 3960
 QY 1321 SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGln 1340

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Db      3961 TCACAGAGTCTCTATGACCAAGCGGTGTCTCTGCTGACCTGGAGAGCGGCTGGAGCTGAG 4020
QY      1341 GYLeuValSer 1344
Db      4021 GGCGTGGTGTCT 4032

RESULT 3
US-10-416-642-3
; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: RAMKUMAR, JayaIaxmi
; APPLICANT: ARVIZU, Chandra
; TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0842.PCT
; CURRENT APPLICATION NUMBER: US/10/416,642
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: 60/249,407
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ. ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3

Alignment Scores:
Pred. No.: 0 Length: 3489
Score: 5756.00 Matches: 1102
Percent Similarity: 95.34% Conservative: 2
Best Local Similarity: 95.16% Mismatches: 0
Query Match: 81.37% Indels: 54
Gaps: 1

US-10-066-521-6 (1-1344) x US-10-416-642-3 (1-3489)
QY      1 MetGluGlyAspIysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
Db      1 ATGAGAGAGACAAATGCTCACTTTTCCAGCTACGGGCTGCAGATGCTGTCTATGAG 60
QY      21 LeuAspIysGluGlnPheGlnThrPheIysGluLeuLeuIysIysSerSerGluSer 40
Db      61 CTAGACAAAGAGAAATTTGAGACATTCAGAGAAATTACTTAAGAGAAATCTTCAGATCG 120
QY      41 ThrThrCysSerIleProGlnPheGlnIleGluAsnIleAsnValGluCysLeuValLeu 60
Db      121 ACCGACAGCTCTATCCAGGTTTGAATCGAGATCCAGATCGATGATGCTGGCACTC 180
QY      61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
Db      181 CTCTTGATAGATTAATTGAGAGATGCTGGCCCTGGCTAGCTCATTAAGATCTTTGAA 240
QY      81 AsnMetAsnLeuArgThrLeuSerGluIysAlaArgAspAspMetIys----- 96
Db      241 AACATGAACCTGGCAACCTCTCTCGAGAGAGCAGGAGATGACATGAAGAAATTCACAGAA 300
QY      96 ----- 96
Db      301 GATTCGTAAGCAAGATGACTGACCAAGACCAAGCAAGAAAGTCCAGAAATTA 360
QY      96 ----- 96
Db      361 TATGCGATGACTAAGCTTATCTGGGGGTGTGACATCTCTGACTCGAATTAATAACAC 420
QY      97 -----LysIleSerGlnAlaMetGluGlnGluGly 106
Db      421 AAGTATGTGGAATTCATCTTCTTTTGCAGAAATTCACAAAGCTATGGAACAGAAAGGT 480

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QY      107 AlaThrAlaIleGluThrGluGlnGluIleSerGlnAlaMetGluGlnGluGlyAla 126
Db      481 GCCACGACGACGACGACGACGAGAAACAAGAAATTTCAAGCTATGGAACAGAAAGTACC 540
QY      127 ThrAlaIleGluThrGluGlnGluIleGlyIleGlyIleAspThrTrpAspTyrIysSerHis 146
Db      541 ACACGACGACGACGACGACGAGAAACAAGACATGAGGTGACATGAGGACCTACAGAGTAC 600
QY      147 ValMetThrIysPheHisGluGlnGluIleAspValArgSerPheGluAsnThrAlaAla 166
Db      601 GTATGACCAAAATTCGCTGAGAGAGATGTCGTCGTGTTTGAACCACTGCTGCT 660
QY      167 AspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArg 186
Db      661 GACTGCGCGGAATGCAACGTTGGCTGGTCTTTGATTCAACGCGTGGGCTTCCGG 720
QY      187 ProArgThrValIleHisGlyIysSerGlyIleGlyIysSerAlaLeuAlaArgArg 206
Db      721 CTTCGACGCGTGGTCTGACGAGAAAGTCAGAAATTTGGGAAATCGGCTCTAGCCAGAAAG 780
QY      207 IleValLeuCysThrAlaGlnIleGlyIleLeuTyrGlnIlePheSerTyrValPhePhe 226
Db      781 ATGCTGCTGTGGGCGCAGGAGGACTTACAGAGAAATGTTCTTCTTCGCTTCTTC 840
QY      227 LeuProValArgGluMetGlnArgIlyIysGluSerSerValThrGluPheIleSerArg 246
Db      841 CTCGCCGTTTGAAGATGACGAGCGGAGAGAGAGAGAGAGTGTCAACAGTTTCATCTCAGG 900
QY      247 GluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeu 266
Db      901 GAGTGGCCACACATCCAGGCTCCGAGGACGAGATCATGCTCCGACACAGAAAGCGTTTG 960
QY      267 PheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAspAspThrIysLeuCys 286
Db      961 TTCACTCATTCACGTTTCGATGACTGGGCTGTCTCTCAACAATGACAAAGCTCTGC 1020
QY      287 LysAspTrpAlaGluIysGlnProPheThrLeuIleArgSerLeuLeuArgIysVal 306
Db      1021 AAGAGCTGGCTGAGAGAGAGCTCCGTTCACTCATACGAGTCTGAGAGAAAGTTC 1080
QY      307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluIysLeuIys 326
Db      1081 CTGCTCCCTGAGTCTCTTCGATGCTGACCGTACAGACGCTGGGACACAGAAAGCTCAG 1140
QY      327 SerGluValIleSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIle 346
Db      1141 TCAAGGTCGTGTCTCCCTGCTTACCTGTTAGTGAAGAAATCTCCGGGAAACAAGATC 1200
QY      347 HisLeuLeuLeuGluIysArgGlyIleGlyGluHisGlnIysThrGlnIysLeuArgAlaIle 366
Db      1201 CACTTGCTCTTAGGCGCGGGAATTGGTAGCATCAAGAAACAAAGGTTGCGTGCATC 1260
QY      367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386
Db      1261 ATGAACAACCGTAGGCTGCTGACCAAGTCCAGAGTCCCGCTGGCTCTTCATCTGC 1320
QY      387 ValAlaLeuGlnLeuGlnAspValIleGlyGluSerValIleProPheAsnGlnThrLeu 406
Db      1321 GTGGCCCTGAGCTGACGAGCGTGTGGGGAAGGCTCCCGCTTCAACCAAGCGCTC 1380
QY      407 ThrGlyLeuHisAlaIlePheValPheHisGlnLeuThrProArgGlyValIleArgArg 426
Db      1381 ACAAGGCTGACCGCGCTTTTGTGTTTCATCACTCAACCCCTGAGGCGTGCAGCGC 1440
QY      427 CysLeuAsnLeuGlnGluArgValIleLeuIysArgPheCysArgMetAlaValGluGly 446
Db      1441 TGCTCAATCTGAGAGAAAGATGTCCTGAACGCTTCTGCGGTATGGCTGGAGGGA 1500
QY      447 ValTrpAsnArgIysSerValPheAspGlyAspAspLeuMetValGlnIlyLeuGlyGlu 466
Db      1501 GTGTGAATGAGAAATGATGTTTGAAGGTGACGATCAAGCTCATGGTTCAAGGACTCGGGAG 1560

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LENGTH: 3926
TYPE: DNA
ORGANISM: Homo sapiens
US-10-216-645-1

Alignment Scores:

Pred. No.:	0	Length:	3926
Score:	5756.00	Matches:	1102
Percent Similarity:	95.34%	Conservative:	2
Best Local Similarity:	95.16%	Mismatches:	0
Query Match:	81.37%	Indels:	54
DB:	6	Gaps:	1

US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

QY 1 MetGluGlyAspIysSerLeuThrPheSerSerTyrGlyLeuGlnIntPyrSLeuTyrGlu 20
DB 1 ATGGAAGGAGACAATGCTCACCCTTTTCCAGCTACGGCTGCAGATGGTGTCTCTATGAG 60
QY 21 LeuAspIysGluGluPheGlnThrPheIysGluLeuLeuIysIysSerSerGluSer 40
DB 61 CTGACAGAGAAAGATTTCAGACATTCAGAGAAATTAAGAAAGAAATCTTCAGATCG 120
QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnIleAsnValGluCysLeuValLeu 60
DB 121 ACCACATGCTCTAATCCACAGTTTGAATCGAGATCCAAACGTGGAATGTCTGGCAGTC 180
QY 61 LeuLeuHisGluTyrTyrGlyValAserLeuValThrIlePheSerIlePheGlu 80
DB 181 CTCTTGATAGATTATGAGCATGCTGGCTGGCTAGCTCATTCATTCATCTTTGAA 240
QY 81 AsnMetAsnLeuArgThrLeuSerGluIysValAspAspAspMetIys----- 96
DB 241 AACTGACCTCGGAAACCTCTCTGGAGAAAGGCAAGGATGACATGAAATAATTCACAGAA 300
QY 96 ----- 96
DB 301 GATCTGAAACGATGATGACCAAGACCAAGAAAGAAAGTCCAGAAATATAA 360
QY 96 ----- 96
DB 361 TATGGCATGACTAAGCTTATCTGGGGGTCTGACATCTCTGACTGAATATAAAC 420
QY 97 -----LysIleSerGlnIleMetGluGlnGlu 106
DB 421 AAGTATGTGAATTCATCTCTCTTTTGGAGAAATTTCAACAGCTATGGAACAAAGGT 480
QY 107 AlaThrIleAlaGluThrGluGluGluIleSerGlnIleMetGluGlnGluVal 126
DB 481 GCCACAGACAGACAGACAGAAAGAAATTCACAAAGCTATGGAACAAAGGTGCC 540
QY 127 ThrIleAlaGluThrGluGlnGluIleHisGluValAspThrThrPhePheSerHis 146
DB 541 ACAGACAGACAGACAGAAAGAAAGCAATGAGGTGACATGGAGCTTACAGAGTAC 600
QY 147 ValMetThrIysPheAlaGluGluGluIleAspValArgArgSerPheGluAsnThrAla 166
DB 601 GTATATGACAAATTCGCTGAGAGAGAGATGATGCTGTAGTTTGAAGAACATCGCTGCT 660
QY 167 AspTyrProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTyrGlyPheArg 186
DB 661 GACTGCGCGGAAATGCAAAAGCTTGCTGCTCTTTTATTCAGACCGGTGGGCTCCGG 720
QY 187 ProArgThrValValLeuHisGlyIysSerGlyIleGlyIysSerAlaLeuAlaArg 206
DB 721 CTTGCGACGGGTGTTTGCACGGAAGTCAGAAATGGAATGGCTTAGCCAGAAAG 780
QY 207 IleValLeuCysTyrAlaGlnGlyIleLeuTyrGlnGlyMetPheSerTyrValPhePhe 226
DB 781 ATGTCGCTGTGCTGGGGGCAAGGTGAGCTTACCAAGGAATGTTCTCTAGCTTCTTC 840
QY 227 LeuProValArgGluMetGlnArgIleValAspIysSerValThrGluPheIleSerArg 246

DB 841 CTCCTCCGTTAGAGATGACGCGAAGAGAGAGACAGTGTCAAGATTCATCTCCAGG 900
QY 247 GluTyrProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeu 266
DB 901 GAGTGGCCAGACTTCCAGAGCTCCGGTGAAGGATCATGTCTCCGACCAAGAAAGGCTGTG 960
QY 267 PheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrIysLeuCys 286
DB 961 TTCATCATTTACGGTTTCATGATGACCTGGGCTGTCTCTCAACATGACACAAAGCTCTGC 1020
QY 287 IysAspTyrAlaGluIysGlnProProPheThrLeuIleArgSerLeuLeuValGlyVal 306
DB 1021 AAGACTGGGCTGAGAAAGACCTCCGTTACCTCATACGAGTGTGTGAGAGAGTTC 1080
QY 307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluIysLeuIys 326
DB 1081 CTGCTCCCTTAGTCTCTTCATGATCTGACCGTTCAGAGACCTGGGGCACAGAAAGCTCAG 1140
QY 327 SerGluValIleSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIle 346
DB 1141 TCAGAGGTGCTGTCTCCCGTACTGTGTAGTGAAGAAATCTCCGGGGAAACAAAGATC 1200
QY 347 HisLeuLeuLeuGluArgGlyIleGlyGluHisGlyIleThrGlnGlnIleAspValIle 366
DB 1201 CACTGTCTCTTGAAGCGGGAATGGTAGACATCAAGAGACAGAGGTTGCTGTGCATC 1260
QY 367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386
DB 1261 ATGAAACACCGTAGCTGCTGACACAGTGCAGAGTCCCGCGGTGCTCTCATATTCG 1320
QY 387 ValAlaLeuGlnLeuGlnAspValValGlyIleSerValAlaProPheAsnGlnThrLeu 406
DB 1321 GTGGCCCTGACGTGACGACGCTGGGGGAAAGGCTCCCGCTTCAACCAACCCCTC 1380
QY 407 ThrGlyLeuHisAlaAlaPheValPheHisGlyLeuThrProArgGlyValValArgArg 426
DB 1381 ACAGGCTTGACCGCTTTTGTTCATCACTCAACCTCGAGGCGTGGTCCGCGC 1440
QY 427 CysLeuAsnLeuGluGluArgValValLeuIysArgPheCysArgMetAlaValGluGly 446
DB 1441 TGTCTCAATCTGAGAGAAAGATTTGCTCTGAAGCGCTTCCGTATGGCTGTGAGAGGA 1500
QY 447 ValIlePheAsnArgIysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGly 466
DB 1501 GTGTGAAATGGAAGTACGTGTTGACGTGACGACTCATGTGTCAAGGACTCGGGAG 1560
QY 467 SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486
DB 1561 TCTAGCTCCGTCTGTGTTTCATGAAACATCTCTTCCAGACGCCACTGTAGAGAG 1620
QY 487 TyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeu 506
DB 1621 TACTACACCTTTCTTCCACCTCACTTCAGAGCTTGTGCTCCGCTGTGACTACGTGTA 1680
QY 507 GluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGlyIysThrIysArgSer 526
DB 1681 GAGGGCTTGAAATCGAGCAGCTCTGCTCTGTACCTTGAGGTTGAGAAAGAAAGGTCC 1740
QY 527 MetGluLeuIysGlnAlaGlyPheHisIleHisSerLeuThrPheIysArgPheLeuPhe 546
DB 1741 ATGAGGCTTAAACAGGAGGCTTCCATATCACTCGCTTGGATGAAGCTTCTTGTGTT 1800
QY 547 GlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValPro 566
DB 1801 GGCTCTGACGAAAGACGTAAGAGGCCACTGAGAGTCTGTGTGGCTGTCCGTTCCC 1860
QY 567 LeuGlyValIysGluIysLeuLeuHisTyrValIserLeuLeuGlyGlnGlnProAsnAla 586
DB 1861 CTGGGGGTGAAGCAAGCTTCTGCACTGGGTCTCTGTGTGGGTCAAGCAAGCTTAAAGCC 1920
QY 587 ThrThrProGluAspThrIleuAspAlaPheHisCysLeuPheGlnThrGlnAspIysGlu 606
DB 1921 ACCACCCCAAGAGACACCTGAGAGCTTCCACTGTCTTTTCAAGACTCAAGACAAAGAG 1980

QY 607 PheValAlaLeuAlaLeuAlaSerPheGlnGluValTrpLeuProIleAsnGluAsnLeu 626
 DB 1981 TTGTTGCTGGCTGGATTAACAAGCTTCCAGAAAGTGGCTCCGATTAAACAAGACCTG 2040
 QY 627 AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
 DB 2041 GACTGTAGATGATCTTCTCTTCCGCTCCAGCATGCTCGTATTGGCGGAAATTCGGGGT 2100
 QY 647 AspValIleGlyIlePheProArgAspGlnSerAlaGluAlaCysProValValProLeu 666
 DB 2101 GATGTCAAGAGGATCTTCCCAAGAGTGAATGCCGTGAGGATGCTGTGGTCCCTCTA 2160
 QY 667 TrpMetArgAspLysTrpLeuIleGlnGluGlnTrpGluAspPheCysSerMetLeuGly 686
 DB 2161 TGGATGGGGATTAAGACCTCTCATTTGAGAGCATGGGAGAAATTTCTGCTCCATGCTTGGC 2220
 QY 687 ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
 DB 2221 ACCCAACCAACACCTGGGCGAGCTGGACCTGGGCGAGCATCTTGACAGACGGGCGCATG 2280
 QY 707 LysThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArg 726
 DB 2281 AAGACCTGTGTGCGCAAGCTGAGGCATCCACCTGCAGATACAGACCTGATGTTTGA 2340
 QY 727 AsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsn 746
 DB 2341 AATGCACAGATTACCTCGTGTGTGAGACCTCTGGAATAATGTCATATGGCCACCGTAA 2400
 QY 747 LeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGluAspValArgMetAlaCys 766
 DB 2401 CTTAAGATCCCTCAACTTGGAGGACCCACCTGAAGAAAGAGATGAAGATGGCGGT 2460
 QY 767 GluAlaLeuLysHisProLysCysLeuLeuGlnSerLeuArgLeuAspCysGlyLeu 786
 DB 2461 GAAGCTTAAACACCCCAAAATGTTGTGTGAGTCTTGAAGCTGATGTGCTGGATTTG 2520
 QY 787 ThrHisAlaCysTyrTrpLeuLysIleSerGlnIleLeuThrTrpSerProSerLeuLysSer 806
 DB 2521 ACCCAATGCTGTATCTTAAGATCTCCCAATCTTACAGACCTCCCAAGCTGAAATCT 2580
 QY 807 LeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeu 826
 DB 2581 CTGAGCCTGGAGGAAACAAGTGAACAACAGGAGATGAAGCCCTCAGATGATCCCTTG 2640
 QY 827 ArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThr 846
 DB 2641 AAGATCTCCAGTGGCGCTCGACAGAACTGATACCTGAGAGACTGTGGCATCACACCG 2700
 QY 847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
 DB 2701 GGTGGCCAGAGTCTGGCTCAAGCCCTCGTCAAGCAACCGAGCTTACACACCTGTGCTTA 2760
 QY 867 SerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
 DB 2761 TCCAAACAAGCTGGGGAAGAGATGAATCTACTGTGTGATCTCAATAGAGCTTCCC 2820
 QY 887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
 DB 2821 CACTGTACTGTGCAAGAGCTGATGTGATCACTGACCACTGACACAGCTGGCTGTGTGT 2880
 QY 907 PheLeuAlaLeuAlaLeuMetClyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
 DB 2881 TTTCTTGACCTGCTTATGGGTACTATGTGTGACGACCTTACGCTTATGACATGAC 2940
 QY 927 ProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgLysProSerCysHis 946
 DB 2941 CCTGTGGAAGACAATGGCGCTGAAGCTTCTGTGCGAGCTCATAGAGAACATCTTGTAT 3000
 QY 947 LeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGlnSerLeuSer 966
 DB 3001 CTCGAGGACCTGGAAGTGGTAAAGTCACTCACCGCGCGTGTGATGAGAGTCTGTCC 3060

QY 967 CysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGly 986
 DB 3061 TGTGTGATCTCGAAGACAGACACCTGAAGAGCTGTGATCTCAAGGACAATGCCCTGGGT 3120
 QY 987 AspGlyGlyValAlaAlaLeuCysGlnGlyLeuLysGlnLysAsnSerValLeuThrArg 1006
 DB 3121 GACGTTGGCTTGTGCACTGTGCAAGAGCTGAAGCAAAAGAACAGGTCTACAGAGA 3180
 QY 1007 LeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeu 1026
 DB 3181 CTCGGGTGAAGGAGATGTGACTGATCTTGTATGCTGTAGAGGACTCTCTTGGCCCTT 3240
 QY 1027 SerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
 DB 3241 TCTGCAACCGGAGATCTGACAGCTTAACCTGGTGCAGATTAATTCAAGCCAAAGGA 3300
 QY 1047 MetCysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeu 1066
 DB 3301 ATGATGAAGCTGTGTGGCTTGTGCTTGCCTGCCACGCTTAATTACATATTTGGGCTG 3360
 QY 1067 TrpLysTrpGlnIleProValGlnIleArgLysLeuGlnGluValGlnLeuLeuLys 1086
 DB 3361 TGAATAAGCAATACCTGTGCATAATAGAACTCTGGAGGAAGTCACTGACTCAAG 3420
 QY 1087 ProArgValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
 DB 3421 CCCGAGTGTATTAATGAAGTGAATGGATTTGGCATTTTGTATGAAGATGACCGGTAC 3474

RESULT 5
 US-10-860-761-3
 ; Sequence 3, Application US/10860761
 ; Publication No. US20040248775A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WYETH
 ; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
 ; FILE REFERENCE: AM101318
 ; CURRENT APPLICATION NUMBER: US/10/860, 761
 ; CURRENT FILING DATE: 2004-06-03
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3
 ; LENGTH: 3885
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3603)
 US-10-860-761-3

Alignment Scores:
 Pred. No.: 0 Length: 3885
 Score: 5741.50 Matches: 1098
 Percent Similarity: 96.16% Conservative: 3
 Best Local Similarity: 95.90% Mismatches: 3
 Query Match: 81.16% Indels: 41
 DB: 8 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-860-761-3 (1-3885)
 QY 1 MetGlnGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
 DB 154 ATGGAAGAGACAATATGCTCACTTTCACAGCTACGAGCTGCAATGTGCTCTATAGAG 213
 QY 21 LeuAspLysGlnGluPheGlnThrPheLysGlnLeuLeuLysLysLysSerSerGlnSer 40
 DB 214 CTAGCAAGAGAAATTTCAACAATTCAGAAATTAAGAAATTAAGAAATTAAGAAATTC 273
 QY 41 ThrThrCysSerIleProGlnPheGlnIleGlnAsnAlaAsnValGluCysLeuAlaLeu 60
 DB 274 ACCACATCTCTATTCCACAGTTTGAATCCAGAAATCCAGAAATCCAGATGCTGGCACTC 333
 QY 61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80

Db	334	CTCTTGCAATGATGATTTATGAGACATCGCTGGCCCTGGGCTACGTCAATTACATCTTTGAA	339
Qy	81	AsmMetAsnLeuAargThrLeuSerGlnIlyalAargAspMetIlySlys-----	97
Db	394	AACATGAACCTGCCAACCCCTCTCGGAGAAAGGCACGGATGACATGAAAACAAATTCAACCA	453
Qy	97	-----	97
Db	454	GAAGATCTCGAAGCAACGATGACTGACCAAGACCAACGAAGAAAAGTGCCAGGAATT	513
Qy	98	-----IleSer	99
Db	514	TCACAAGCTGTCACAAAGATAGTGCACAGCTCCAGACACAAAGAACAGGAATTTC	573
Qy	100	GlnAlaMetGlnGlnGlnIlyalAThrAlaIagIuthrGlnGlnGlnIlyIleSerGln	119
Db	574	CAACCTATGAAACAAGAAAGTGCCACAGACGACAGACAGAAACAAGAAATTTCACAA	633
Qy	120	AlaMetGlnGlnGlnIlyalAThrAlaIagIuthrGlnGlnGlnIlyIleGlyIlyAsp	139
Db	634	GCTATGGAAACAAGAAAGTGCCACAGACGACAGACAGAAACAAGAACATGGAGGTGAC	693
Qy	140	ThrTrpAspTrpIlySerSerIleValMetThrIlySerPheAlaGlnIlyGlnIlyAspValArg	159
Db	694	ACATGGGACTCAAGATGACGATGATGACCAAAATTCGTGACGAGAGATGTACGTCT	753
Qy	160	SerPheGlnuAnthrAlaAlaAspTrpProGlnuMetGlnThrLeuAlaGlyAlaPheAsp	179
Db	754	AGTTTGAACCACTGCTGCTGACTGGCCGGAATGCAACGTTGGCTGGCTTTGAT	813
Qy	180	SerAspAspTrpGlyPheAspProAspThrValIleuHisGlyIlySerGlyIleGly	199
Db	814	TCAGACCCGTGGGGCTTCCGGCTTCGACGGTGGTTCGACGGAAGATCGAAGATTGGG	873
Qy	200	LysSerAlaLeuAlaArgArgIleValIleuCysTrpAlaGlnIlyGlyIleuTrpGlnIly	219
Db	874	AAATGGCTCTAGCCAGAAAGATGTGCTGTGGCGCAGGTGCACTTCCACAGGA	933
Qy	220	MetPheSerTrpValPhePheLeuProValArgIluMetGlnArgIlySlyGlnSerSer	239
Db	934	ATGTTCTCTCAAGTCTTCTCTCCCGTTAGAGAGATGACGCGGAAGAAAGACAGCAGT	993
Qy	240	ValThrGlnPheIleSerArgGlnTrpProAspSerGlnAlaProValThrGlnIleuMet	259
Db	994	GTCACAGAGTTCATCTCCAGGGAAGTGGCCAACTCCCGCTCCGGTGCAGGAATCATG	1053
Qy	260	SerArgProGlnuArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValIleu	279
Db	1054	TCCCAACCAAGAAAGCTGTGTTCATCATTAACGGTTCATGACGTGGGGCTCTGTCTTC	1113
Qy	280	AsnAsnAspTrpIlySlyCysIlyAspTrpAlaGlnIlySglnProPheThrLeuIle	299
Db	1114	AACATATGACAAAGCTCTGCAAGACCTGGGCTGAGAGACGCTCCGTTCACTCATTA	1173
Qy	300	ArgSerLeuLeuArgIlyValIleuLeuProGlnSerPheLeuIleValThrValArgAsp	319
Db	1174	CGAGATCTGATGAGGAAGTCTCGTCTCCCTGAGTCTTCCGTATCGTCAACGTCAGAGAC	1233
Qy	320	ValGlyThrGlnIlySlyLeuIlySerGlnuValIleSerProAspTrpLeuLeuValArgIly	339
Db	1234	GTTGGCAACAGAAAGCTCAAGTCAGAGGTGTGTCTCCCGTATCCGTGTAGTAGGA	1293
Qy	340	IleSerGlyIlyGlnIlyArgIleHisIleuLeuLeuGlnArgIlyIleGlyIlyuHisGlnIlyS	359
Db	1294	ATCTCCGGGGCAACAAGATCACTGTCTCTTAGCGCGGGATTGGTAGACATCAAGAG	1353
Qy	360	ThrGlnIlyLeuArgAlaIleMetAsnAsnArgGlnLeuLeuAspGlnCysGlnValPro	379
Db	1354	ACACAAAGGTTGCGGCGATCATCAACAACCGTAGCTGTCCACAGTGCACAGTGC	1413
Qy	380	AlaValGlySerLeuIleCysValAlaLeuGlnIleuGlnAspValValGlyIlyuSerVal	399
Db	1414	GCCGTGGGCTCTCTATCTGGCTGGCCCTTGACGTGCAGAGACGTGGTGGGAGAGCGCTC	1473

QY	400	AlaProhPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr	419
DB	1474	GCCCCCTTCAACCAAGGCTCACAAGGCTGACGCGCCTTTGGCTTTCATCACTCAACC	1533
QY	420	ProArgGlyValValAlaArgArgCysLeuAsnLeuGlnGluValValLeuLysArgPhe	439
DB	1534	CCTGAGGCGGTGGTCCGGCGCTGGTCAATCTGGAGGAAAGAGTGTCTGGAAGCGCTTC	1593
QY	440	CysArgMetAlaValGlnGlyValTTPAsnArgLysSerValPheAspGlyAspAspLeu	459
DB	1594	TGCCGTATGGCTGTGGAGGAGGTGTGAATAAGAAAGTCAAGTGTTAATGGTGAAGACTC	1653
QY	460	MetValGlnGlyLeuGlnGlyLysSerGlnLeuArgAlaLeuPheHisMetAsnIleLeuLeu	479
DB	1654	ATGGTTCAGAGACTCGGAGAGCTGAGCTCGAGTCTGGTTCACATGAACATCTTCTTC	1713
QY	480	ProAspSerHisCysGlnGluGlyTyrTTPhePheHisLysSerLeuGlnAspPheCys	499
DB	1714	CCACACAGCCACTGTGAGAGATTAACACTTCTTCCACCTCAAGTCTCCAGAACTTCTGT	1773
QY	500	AlaAlaLeuTyrTyrValLeuGlnGlyLeuGlnIleGluProAlaLeuCysProLeuTyr	519
DB	1774	GCCCCCTGTGTACTAGTGTATGAGGGGCTGGAAATTCAGAGCAAGCTCTTGGCCCTGTAC	1833
QY	520	ValGlnLysThrLysArgSerMetGlyLeuLysGlnIleGlyPheHisLysHisSerLeu	539
DB	1834	GTTAGAGACAAAGAGGCTCCATGAGCTTTAAACAGCAGGCTTCCATATCCACTCGCTT	1893
QY	540	TrpMetLysArgPheLeuPheGlyLeuValSerGlnAspValAlaArgArgProLeuGlnVal	559
DB	1894	TGATGAAGACGTTTCTTGTTGGCTCGTGTAGCAAGACGTAAAGAGAGGCCACTGAAGTCC	1953
QY	560	LeuLeuGlyCysProValProLeuGlyValIleGlnLysLeuHisIleTPValSerLeu	579
DB	1954	CTGCTGGGCTGTCCCGTCCCTCGGCTGGAGGAGAAAGCTTGCACCTGGGATCTCTGTG	2013
QY	580	LeuGlyGlnGlnProAsnAlaThrTTProGlyAspThrLeuAspAlaPheHisCysLeu	599
DB	2014	TTGGGTCAAGCAAGCTTAATGCCACCCACAGAAACACCTCGAGACGCTTCCACTGTCTT	2073
QY	600	PheGlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsnSerPheGlnGlnValTTP	619
DB	2074	TTTCGAGACTCAAGCAAAAGATTGTTGGCTTGGCAATTAAACACTTCCAAAGAGTGTGG	2133
QY	620	LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro	639
DB	2134	CTTCCGATTAAACCAAGACCTGGAAGCTTAATACACTTCTCTTCTCCACAGACTGTCCG	2193
QY	640	TyrLeuArgLysIleAspValAspValLysGlyIlePheProArgAspGlySerAlaGlu	659
DB	2194	TATTTGCCGAAAAATTCGGGTGAGATGTCAAGGGATCTTCCAAAGATGATCCGCTGAG	2253
QY	660	AlaCysProValValProLeuTTPMetArgAspLysThrLeuIleGlnGlnTTPGlu	679
DB	2254	GCATGTCTGTGGTCCCTCTATGATGGAGGAGATTAAGACCTCATTTGAGAGCACTGGGAA	2313
QY	680	AspPheCysSerMetLeuGlyTTPHisIleProHisLeuAspArgGlnLeuAspLeuGlySerSer	699
DB	2314	GATTTCTGTCTCCATGCTTGGACCAACCCCAACCTCGCGGAGCTGGAGCTTGGAGCAAGC	2373
QY	700	IleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisIleTPThrCysLys	719
DB	2374	ATCTCGACAGAGCGGGCCATGAACACTGTGTGCCAAGCTGAAGGCATCCCACTGGAG	2433
QY	720	IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTTPArg	739
DB	2434	ATACAGACCTCGATGTTTAGAAATGCAACAGATTACCCCTGGTGTGCAACACTCTGGAGA	2493
QY	740	IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleTTPHisLeuLysGlu	759
DB	2494	ATGTGCATGGCCAACTGTAACTTAAGTCCCTCAACTTGGAGAGCAACCACTGAAGGAA	2553

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QY 760 G1uapValaIarMetAlaCyGluAlaLeuYshIspProLysCyBLeuLeuG1uSerLeu 779
DB 2554 GAGATGTAAAGATGGCTGTGAAGCTTTAAACCCAAAATGTTTGTGAGCTTTG 2613
QY 780 ArgLeuapCyCyGlyLeuThrIshAlaCyGlyLeuYshIleSerGlnIleLeuThr 799
DB 2614 AGGCTGAGTTCCTGTGATTAACCAATGCTGTATCTGAAGATCTCCAAATCTTACG 2673
QY 800 ThierProSerLeuYserLeuSerLeuAlaGlyValLeuYshValThrArgGlnIVal 819
DB 2674 ACCCTCCCAACCTGAATCTCTGAGCTGAGGAAACAAAGTGAACAGGAGGAGTA 2733
QY 820 MetProLeuSerAapAlaLeuArgValSerGlnCyValAlaLeuGlnIleLeuGln 839
DB 2734 AGGCTCTCAATGATGCTTTAAGGCTCTCCAGTCCGCTCCAGAACTGATCTGAG 2793
QY 840 AapCyGlyIleThrAlaThrGlyCyGlnSerLeuAlaSerAlaLeuValSerAapArg 859
DB 2794 GACTGTGACATCAAGCCAGCGGTGCGAGAGTCTGGCCTCAGCCCTGTCAGCAACCG 2853
QY 860 SerLeuThrIshLeuCyLeuSerAapAapSerLeuGlyValLeuGlnIValAapLeu 879
DB 2854 AGCTTGACACACCTGTGCTATCCAAACAGCTGGGGAACGAAGGTGAATCTACTG 2913
QY 880 CysArgSerMetArgLeuProIshCySerLeuGlnArgLeuMetLeuAapGlnCyshIsh 899
DB 2914 TGTGATCATAGAGCTTCCCACTGATGCTGCAAGAGCTGATCTGATCAAGTCCAC 2973
QY 900 LeuAapThrAlaGlyCyGlyPheLeuAlaLeuAlaMetGlyAapSerTrpLeuThr 919
DB 2974 CTGAGCAGCGCTGGTGTGTTCTCTTGCACCTTGCACTTGAGTAACCTAGCTGAGCG 3033
QY 920 H1aLeuSerLeuSerMetAapProValGluAapAapGlyValLeuLeuLeuGlnVal 939
DB 3034 CACCTGAGCTTGAATGAACCTGTGTGAAGCAATGCGGTGAACCTTGTGTCAGGTC 3093
QY 940 MetArgGlnProSerCyshIshLeuGlnAapLeuGlnLeuValIshCyshIshLeuThrAla 959
DB 3094 ATGAGAAACCATCTTGTATCTCAAGACCTGAGGTTGTGAAGTGTCAATCTCACCC 3153
QY 960 AlaCyGlySerLeuSerCyValIleSerArgSerArgIshLeuYshSerLeuAap 979
DB 3154 GCGTCTGTGAAGCTGTCTGCTGTGATCTGAGAGAGACACCTGAAGAGCTGAGT 3213
QY 980 LeuThrAapAapAlaLeuGlyAapGlyValAlaAlaLeuCyGlnGlyLeuYshGln 999
DB 3214 CTCAAGGACAAATGCGCTGGGTGAACGCTGGGTGTGCTGTGAGGAGCTGAAGCA 3273
QY 1000 LysAapSerValLeuThrArgLeuGlyLeuYshAlaCyGlyLeuThrSerAapCysh 1019
DB 3274 AAGAAACATGTTCTGACAGACTCGGGTTGAAGGCAATGACATCTTGTGATTCGT 3333
QY 1020 GluAlaLeuSerLeuAlaLeuSerCyAapAapArgIshLeuThrSerLeuAapLeuValGln 1039
DB 3334 GAGGACCTCTCTTGGCCCTTTCTGCAACCGGCACTGACCAAGCTGAACCTGAGG 3393
QY 1040 AapAapPheSerProGlyIshMetLeuYshLeuCySerAlaPheAlaCyProThrSer 1059
DB 3394 AATACTTCAGTCCCAAGAAATGAATGAAGCTGTGTGCGCTTGGCTGTCCACGCT 3453
QY 1060 AapLeuGlnIleIleGlyLeuThrPlySerTrpGlnIshProValGlnIleArgYshLeu 1079
DB 3454 AACTTACATATATGGCTGTGAAATGCGACGTACCTGTGCAATTAAGAACTGTG 3513
QY 1080 GluGluValGlnLeuLeuYshProArgValValIleAapGlySerTrpIshSerPheAap 1099
DB 3514 GAGGAAGTGAGCTACTGAAGCCCGAGTGGTAATTAAGGTAAGTGGCATCTTTGAT 3573
QY 1100 GluAapAapArgIshIsh 1104
DB 3574 GAAGATGACCGGTAC 3588

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RESULT 6

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US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US2004002869A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 56.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
DB: 7 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-399-443-23 (1-3900)
QY 1 MetGluGlyAapLysSerLeuThrPheSerSerTrpGlyLeuGlnIshTrpCyLeuTrpGlu 20
DB 154 ATGGAAGAGACAAATGCTCACCCTTTCAGCTACGCGGTGCAATGTGTCTATAG 213
QY 21 LeuAapLysGluGlnPheGlnIshPheYshGluLeuLeuYshYshSerSerGlnSer 40
DB 214 CTAGCAAGAAAGAAATTCAGACATTCAGAGAAATTAAGAAAGAAATTCAGAAATCG 273
QY 41 ThrThrCySerIleProGlnPheGlnIshGluAapAlaAapValGluCyLeuAlaLeu 60
DB 274 ACCACATCTCTATTCACAGATTGAAATCGAATGCAACGCGAATGTCTGCACTC 333
QY 61 LeuLeuIshGluTrpGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGln 80
DB 334 CTCTTGATGATGATTAATGAAGCAATGCTGGCTGGCTGAGTCAATTAAGATCTTGA 393
QY 81 AapMetAapLeuArgThrLeuSerGlyValAapAapAapMetLeuYsh----- 97
DB 394 AACATGAACCTGCGAACCTCTCGGAAGAGCAAGGATGACATGAAGAAACATTCACCA 453
QY 97 ----- 97
DB 454 GAAGATCTTGAAGCAACATGATGACCAAGACCAAGCAAGAAAGATGCCAGAAAT 513
QY 98 -----IleSer 99
DB 514 TCACAAAGTGTGCAACAAATAGTGCACAGCTGCAGAGCAAAAGAACAGGAATTTCA 573
QY 100 GlnAlaMetGluGlnGlnGlyValAlaThrAlaIshGlnIshGlnIshSerGln 119
DB 574 CAAGCTATGAAACAAAGAGGTGCCACAGCAGACAGAGCAAGAAAGAAATTTCAACA 633

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QY	120	AlaMetGluInglInglValaThraIaIaGluThrGluInglInglValhISglYGLyAsp	139
Db	634	GCTATGGAACAAGAAAGTGCCACAGACACAGACAGAAAGAACAGACATGAGGTGAC	693
QY	140	ThrTPAAspYrYLYsSerHisValMetThrLYsPheIaGluGluAspValArgArg	159
Db	694	ACATGGAGCTACAGAGCTCACGTATGACAAATTGCTGAGAGAGAGATGTCGTCT	753
QY	160	SerPheGluAsnThrIaIaIaAspTPProGluMetGlnThrLeuIaGlyValaPheAsp	179
Db	754	AGTTTGAACAACTGCTGTGACTGGCCGGAATATGCAAAAGTTGGCTGTGCTTTGAT	813
QY	180	SerAspAspTPrgLYPheArgProArgThrValValaLeuHISglYLYsSerGlyTIGly	199
Db	814	TCAAGCCGGTGGGGCTCCGGCTCGACAGGTGGTTCTGCACGGAATCGAGAAATTCGAAATTTGGG	873
QY	200	LYsSerIaIaLeuIaIaArgArgIleValLeuCYsTPAaGlnGlyLYsLeuTYGlnGly	219
Db	874	AAATGGGCTTACGCCAAGAGATCGTGTCTGGGGCAAGGTGACCTTACAGGGA	933
QY	220	MetPheSerTYValaPhePheLeuProValaArgGluMetGlnArgLYsGluSerSer	239
Db	934	ATGTTCTCTACGTCTTCTTCTCCCGCTAGAGAGATGACGCGGAAGAAAGAGAGCAGT	993
QY	240	ValThrGluPheIleSerArgIuThrProAspSerGlnaIaProValaThrGluIleMet	259
Db	994	GTCACAGAGTTCAATCTCCAGAGAGGGACAGCTCCACGGCTCCGGTACAGAAATCAATG	1053
QY	260	SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu	279
Db	1054	TCCGACCAAGAAAGCTGTGTTTATCATTTGACGGTTTCGATGACCTGGGCTCTGTCTC	1113
QY	280	AsnAsnAspThrLYsLeuCYsLYsAspTPAaGluLYsGlnProProPheThrLeuIle	299
Db	1114	AAACATGACACAAACCTCTGCAGAAACATCGGGGTGAGAGAGCGCTCCGTTACCCCTCATTA	1173
QY	300	ArgSerLeuLeuArgLYsValleuLeuProGluSerPheLeuIleValaThraIArgAsp	319
Db	1174	CGCACTCTGCTGAGGAGAGGTCTCTGCTCCCTGAGTCTTCGATCGTACCGTACAGAGAC	1233
QY	320	ValGlyThrGluLYsLeuLYsSerGlyValaIaSerProArgTYrLeuLeuValArgGly	339
Db	1234	GTTGGACAGAAACCTCAAGTCAGAGGTCGTGTCTCCCGTTACTGTATGTTAGAGGA	1293
QY	340	IleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyValhISglLYs	359
Db	1294	ATCTCGGGGAAACAAGATCACTGCTCTCTTGAAGCGGGGATTGGTGAACATCAAGAG	1353
QY	360	ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCYsGlnValPro	379
Db	1354	ACACAAAGGGTTGCGGCATCTCAACAACCGTGAAGCTCGACACATGTGCCAAGGTGCC	1413
QY	380	AlaValaGlySerLeuIleCYsValaIaLeuGlnLeuGlnaAspValaGlyGluSerVal	399
Db	1414	GCGGGGGCTCTCTCATCTGCGGGCCCTTGACGCTGCAGAGACGTGTGGGGAGAGCCTC	1473
QY	400	AlaProPheAsnGlnThrLeuThrGlyLeuHisIaIaIaPheValaPheHisGlnLeuThr	419
Db	1474	GCCCCCTTCAACCAACGCTCACAGGCTGCACGCGGCTTTTGGCTTTCATCAAGTCAACC	1533
QY	420	ProArgGlyValaIArgArgCYsLeuAsnLeuGluArgValaIleuLYsArgPhe	439
Db	1534	CCTCAGAGCGTGGTCCGGCGCTGTCTCAATCTGAGAGAAAGTTGTCTGAAGCGCTTC	1593
QY	440	CysArgMetAlaValaGluGlyValaIThrAsnArgLYsSerValaPheAspGlyAspAspLeu	459
Db	1594	TGCCCTAATGGCTGTGAGAGGAATGGAAATGGAATGATGTTGAATGTCAGCACTTC	1653
QY	460	MetValaGlnGlyLeuGlyGluSerGlyLeuLeuArgAlaLeuPheHisMetAsnIleLeuLeu	479
Db	1654	ATGGTTCAAGACCTCGGGAGGTCTAAGCTCCGTGCTCTGTTTCACATAGACATCTCTTTC	1713
QY	480	ProAspSerHisCYsGluGluIuTYrTYrThrPhePheHisLeuSerLeuGlnAspPheCYs	499

Dd	1714	CCAGAGACCACTGGAGAGATACACACTTCTTCCACTCCTACGCTCCAGGACTTCTGT	1772
Qy	500	AlaAlaLeuTyTYrValLeuGluGlyLeuGluIleGluProAlaLeuCybProLeuTy	519
Dd	1774	GCCGCGCTGTACTACGTGTAGAGGGCCGTGGAAATCGAGCCAGCAAGCTCTGTGCCCTGTGAC	1833
Qy	520	ValGluTyThrIleValArgSerMetGluLeuLeuysGlnIleaglYrPheNileIleIsSerLeu	539
Dd	1834	GTTGAGAAAGACAAAGAGGTCCATGGAGCTTTAAACAGGAGGCTTCCATATCCACTCGCTT	1891
Qy	540	TrpMetIleValArgPheLeuPheGlyLeuValIserGluAspValArgArgProLeuGluVal	559
Dd	1894	TGGATGAAGCGTTTCTTGTGTGGCTCTGTAGCCGAAGACGTAAAGAGGCCACTGAGAGGTC	1951
Qy	560	LeuLeuGlyCybProValProLeuGlyValIlySGluIlyIleuLeuNileTrpValIserLeu	579
Dd	1954	CTGCTGGGCTGTCCCGTTCCTCCCTGGGGGTGAAGCAAGAGCTTCTCACTGGGCTCTCTCG	2011
Qy	580	LeuGlyGlnIleProAsnAlaThrThrProGlyAspThrIleuAspAlaPheNileCybLeu	599
Dd	2014	TTGGGTCAAGACGCTTAATGCCACACCCCAAGAGACACCTTGAGAGCCCTTCCACTGTCTT	2072
Qy	600	PheGluThrGluAspIlyGluPheValArgLeuAlaLeuAsnSerPheGlnIleValITrp	619
Dd	2074	TTTCGAGACTCAAGACAAAGAGTTGTGTGCTGGCATTTAAACAGTTCCAAAGATGTGTG	2133
Qy	620	LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCybLeuGlnIleCybPro	639
Dd	2134	CTTCCGATTTAACAGAACCTGGACTTGAATAGCATTTCTTCTGTGCTCCAGACCTGTCCG	2199
Qy	640	TyrLeuArgIyIleArgValAspValIlySGlyIlePheProArgAspGluSerAlaGlu	659
Dd	2194	TATTTCGCGAAATATCGGTGGATGTCAAGAGGATCTTCCCAAGAGATGAGTCCGCTCGAG	2253
Qy	660	AlaCybProValValProLeuITrpMetIlyArgAspIlyThrIleIleGluGlnGluITrpGlu	679
Dd	2254	GCATGTCTGTGGTCCCTCTCTAGTAGAGTGGGATTAAGACCTCATTAAGAGAGCAGTGGGA	2311
Qy	680	AspPheCybSerMetLeuGlyIThrNileProNileuValGlnIleuAspLeuGlyIserSer	699
Dd	2314	GATTTCTGTCTCAATGCTTGGCACCCACCCACACCTGGGCGAGCTGAGCTGGGCGAGCTC	2372
Qy	700	IleLeuThrGluArgAlaMetIlyThrIleuCybAlaIlyIleuArgNileProThrCybIys	719
Dd	2374	ATCTCGACAGAGCGGGCCATGAAAGCCCTGTGTGCAGGCTGAGGCACTCCACCTGGCAG	2433
Qy	720	IleGlnIThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnIleIleuITrpArg	739
Dd	2434	ATACAGACCTCGATGTTTAAATACACAGATTACCCCTGGTGTCCACAACCTCTGGAGA	2491
Qy	740	IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIlyIThrNileuIlySGlu	759
Dd	2494	ATCGTCATGGCCCAACGTAACTTAAGATCCCTCAACTTGGGAGGACCCACCTGAAGGA	2551
Qy	760	GluAspValArgMetAlaCybGlnAlaIleuIlyNileSProlysCybLeuGluIlySerLeu	779
Dd	2554	GAGGAGTGAAGATGCGGTGTGAACCTTTAAACACCCAAATGTTGTGTGAAGTCTTTG	2611
Qy	780	ArgLeuAspCybCybGlyLeuIThrNileIsAlaCybITyLeuIlyIleIserGlnIleLeuIThr	799
Dd	2614	AGGCTGAGTTGTGTGATTAAGCCATGCTGTTCATCGAAGATCTCCCAATCTCTAAG	2672
Qy	800	ThrSerProSerLeuIlySerIleuSerIleuAlaGlyAsnIlyValIThrAspGlnIlyVal	819
Dd	2674	ACCTTCCCCCAGGCTGAATATCTCTGAGCTTGGAGGAAACAAGTGAACAACAAGGAGAGA	2733
Qy	820	MetProLeuSerAspAlaLeuArgValIserGlnCybAlaLeuGlnIlyLeuIleIleuGlu	839
Dd	2734	ACGCTCTCAAGTGAAGCTTTGAAGGATCTCCAGTGCCTGCAAGACTGATATCTGGAG	2791
Qy	840	AspCybGlyIleThrAlaIThrGlyCybGlnSerIleuAlaSerAlaLeuValIserAsnArg	859

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Db 2794 GACTGTGCATCACAGCAGGGTTGCGAGAGTCTGACCTGACCGCTGTGACGACCGG 2853
Qy 860 SerLeuThrhAlaLeuCybLeuSerAsnAsnSerLeuGlyValAlaAsnLeu 879
Db 2854 AGCTTGACACACCTGTGCTATTCACAAACAGCCGTGGGAAAGAAAGTGAATCTACTG 2913
Qy 880 CysArgSerMetCysLeuProHicCysSerLeuGlnatgLeuMetLeuAsnGlnCysHic 899
Db 2914 TGTGATTCATGAGGCTTCCCACTGATGCTGACAGAGCTGATGCTGATCAAGTCCAC 2973
Qy 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTriLeuThr 919
Db 2974 CTGACACGCGCTGGTGTGTTCTTCTTCTGACTTGGCTTATGAGTAATCAATGCTGACG 3033
Qy 920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleLeuLeuCybGlyVal 939
Db 3034 CACCTGAGCCTTAGATGATACCCCTGTGAAACATGAGCGTGAACCTTCTGTGACAGGTC 3093
Qy 940 MetArgGluProSerCysHicLeuGlnAspLeuGluLeuValIleCysHicLeuThraIa 959
Db 3094 ATGAGAGAACCATTTTGTCAATCTCCAGACCTGAGATTGTAAGTGTCACTCACCGCC 3153
Qy 960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHicAlaLeuIleSerLeuAsp 979
Db 3154 GCGTGTCTGTGAGAGTCTGTCTCGTGTGATCTCGAGAGACAGACACTGAAAGCTGTGAT 3213
Qy 980 LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCybGlyIleLeuGln 999
Db 3214 CTCACGGAACAATGCGCTGTGACGCTGGGGTGTGCTGTGCTGTGAGAGGACTGAAAGCA 3273
Qy 1000 LysAsnSerValIleLeuThraIleGlnIleLeuLysAlaCysGlyLeuThraSerAspCysCys 1019
Db 3274 AAGAACAGTGTCTGACAGACTCGGGTTGAAGGATGAGATGACTGATCTTGATTCGTCT 3333
Qy 1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHicIleLeuThraSerLeuAsnLeuGln 1039
Db 3334 GAGGAGCTCTCTTGGCCCTTTCCTGCAACCGGACTGACCAAGCTAACTGATGAG 3393
Qy 1040 AsnAsnPheSerProIleGlyIleMetIleLeuCybSerAlaPheAlaCysProThrSer 1059
Db 3394 AATAACTTCAGTCCCAAGAGATGATGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 3453
Qy 1060 AsnLeuGlnIleIleGlyLeuThraIlePheIleProValGlnIleArgIleLeu 1079
Db 3454 AACTTACATATTTGGCTGTGAAATGCAATGCACTTGTCAATTAAGAGCTGTG 3513
Qy 1080 GluGluValGlnLeuLeuLysProArgValIleAspGlySerTriHicSerPheAsp 1099
Db 3514 GAGGAGGTCAGCTACTCAAGCCCGAGTCGTAATTTGACGTAATTTGCAATTTTGTAT 3573
Qy 1100 GluAspAspArgHic 1104
Db 3574 GAAAGTGAACCGGTAC 3588

RESULT 7
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: Represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981

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; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
US-10-677-943-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 96.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
DB: 7 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-677-943-23 (1-3900)

Qy 1 MetGluGlyAspIleSerLeuThraPheSerSerTriGlyLeuGlnTriPheLeuTriGlu 20
Db 154 ATGAGAGAGAGCAATATCCCTCACTTTCAGCTAACGGGCTGCAATGGTGTCTATGAG 213
Qy 21 LeuAspIleGluGluPheGlnThraPheGlyLeuLeuLysIleSerSerGluSer 40
Db 214 CTAGCAAGAGAAATTTCAACATTCAGAAATTACTTAAGAAAGAAATCTTCAGAAATCG 273
Qy 41 ThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db 274 ACCACATCTCTATTTCCACAGTTTGAATCGAAGATCCAAAGTGAATGTCTGCACTC 333
Qy 61 LeuLeuHicGlyTriGlyValSerLeuAlaTriPheIleSerIlePheGln 80
Db 334 CTCTTGCAATGATTAATGAGAGCATCGCTGGCTGTGGCTGATTCATTAATGATTTTGA 393
Qy 81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspMetIleLys----- 97
Db 394 AACATGAACCTCGAACCCTCTCGAAGAGCGAGATGACATGAAGACATTCACCA 453
Qy 97 ----- 97
Db 454 GAAAGTCTGAAGCAAGATGATGACCAAGGACCAAGAAAGAAATGCCAGAAAT 513
Qy 98 -----115Ser 99
Db 514 TCACAACTGTGCAACAAGATAGTCCACAGCTGACAGACAAAGAAACAGGAAATTTCA 573
Qy 100 GlnAlaMetGluGlnGluGlyValaIleThraIaIleGluThraGluGlnIleSerGln 119
Db 574 CAAGCTATGAACAAGAGGTGTCACAGACAGAGACAGAAAGAAAGAAATTTCAACA 633
Qy 120 AlaMetGluGlnGluGlyAlaIleThraIaIleGluThraGluGlnIleHicGlyIleAsp 139
Db 634 GCTATGAAACAAGAGGTGCCACAGCAGACAGAGACAGAAAGACATGAGATGAC 693
Qy 140 ThrTrpAspTriLysSerHicValMetThrIlePheAlaGluGluGluAspValArg 159
Db 694 ACATGGAGCTACAAAGATGACAGTATGACCAAAATTCGTGAGAGAGAGATGTAGCTGT 753
Qy 160 SerPheGluAsnThrAlaIleAspTriProGluMetGlnThraLeuAlaGlyAlaPheAsp 179
Db 754 AGTTTGAACAACATGCTGTGACTGCGCGGAAATGCAACCTTGGCTGTCTTTGAT 813
Qy 180 SerAspArgTriPheArgProArgThraValIleLeuHicGlyLysSerGlyIleGly 199
Db 814 TCAGACCGGTGGGCTTCCGCTGCAAGGTGTCTGACAGGAAAGTGAATTTGGG 873
Qy 200 LysSerAlaLeuAlaArgArgIleValIleuCybTriPheAlaGlnGlyIleLeuTriGlnGly 219
Db 874 AAATCGGCTGTGACAGAGATCGTGTGCTGTGGGCGCAAGGTGACTTACAGGGA 933

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QY 220 MetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSer 239
Db 934 ATGTTCTCCACAGCTCTTCTCTCCCGTTAGAGAGATGCAAGCGGAGAGAGAGAGAGAGT 993
QY 240 ValThrGluPheIleSerArgGluTyrProAspSerGlnAlaProValThrGluIleMet 259
Db 994 GTCAAGAGATTCACTCCAGAGAGTGGCCAGACTCCAGAGCTCCGCTGAGCGAGATCATG 1053
QY 260 SerArgProGluArgLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279
Db 1054 TCCGACCAAGAAAGCGTGTGTTGATGACGGTTTCAGATGACCTGGGCTCTGTCTTC 1113
QY 280 AsnAsnAspThrLysLeuCybLysAspTyrAlaGluLysGlnProProPheThrLeuIle 299
Db 1114 AACCAATACACAAAGCTCTGCAGAAAGCTGGGCTGAGAGAGAGAGAGAGAGAGT 1173
QY 300 ArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319
Db 1174 CGCAGTCTGCTGAGAGAGTCTGCTCCCTGAGTCTTCTGATCTGACCGTCAAGAGAG 1233
QY 320 ValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGly 339
Db 1234 GTGGGCAAGAGAGAGCTCAAGTCAAGAGTGTCTCCGTTACCTGTAGTGAAGA 1293
QY 340 IleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLys 359
Db 1294 ATCTCCGGGAGAACAAAGATCCACTTGTCTTGAAGCGGGAGATGGTGAAGCATCAAG 1353
QY 360 ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValPro 379
Db 1354 ACAAGAGGTTGCGTGTGATCATCAACACCGTGAAGTGTCTGACGAGTCCAGAGTCCC 1413
QY 380 AlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerVal 399
Db 1414 GCGGTGGGCTCTCTCATCTGTGGTGGCTTGCAGCTGACGAGAGTGTGGGGAGAGGCTC 1473
QY 400 AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr 419
Db 1474 GCCCCTTCAACCAAGCGCTCAAGGCGTGCAGCGCGCTTTGGGTTTCAATCAGCTCAC 1533
QY 420 ProArgGlyValValAlaArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPhe 439
Db 1534 CCTCGAGCGGTGTGCGCGCTGTCTCAATCTGAGAGAAAGTGTGCTCGAAGCGGCTTC 1593
QY 440 CysArgMetAlaValGluGlyValTyrAsnArgLysSerValPheAspGlyAspAspLeu 459
Db 1594 TGCCTATGGCTGTGAGAGAGGTGTGGAATGAGAGTCAAGTGTGATGGTACGAGCTTC 1653
QY 460 MetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479
Db 1654 ATGGTTCAAGGAGCTCGGGAGTCTGAGCTCGGTCTGTGTTTCAATGAACATCTTCTTC 1713
QY 480 ProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCys 499
Db 1714 CCGAGACGCGACACTGTGAGAGTACTACACTTCTTCCACCTCAAGTCTCCAGAGCTTCGT 1773
QY 500 AlaAlaLeuTyrTyrValIleuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyr 519
Db 1774 GCGGCTTGTGCTACGATGATGAGAGGCTTGGAATCCAGCCAGCTCTCTGCTCTGTAC 1833
QY 520 ValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisLeuSerLeu 539
Db 1834 GTTGAGAGAGCAAGAGAGTCCATGAGACTTAAACAGGCAAGGCTTCCATATCTCACTGCTT 1893
QY 540 TyrMetLysArgPheLeuPheGlyLeuValSerGluAspValAlaArgArgProLeuGluVal 559
Db 1894 TGGATGAAGGGTTCCTGTGTGGCTGTGTGAGCGAAGACGTAAAGAGAGCCCATGGAAGTCT 1953
QY 560 LeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTyrProValSerLeu 579
Db 1954 CTGCTGGAGCTGTCCCGTTCCCTGGGGGTGAAGAGAGTCTTCTGCACTGGGTTCTCTCTG 2013

QY 580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599
Db 2014 TTGGGTTCAGAGCGCTAATGCTCACACCCGAGAGACACCTTGAGCGCTTCTCCACTGTCTT 2073
QY 600 PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTyr 619
Db 2074 TTGAGAGCTAAGACAAAGAGTGTGTGCTTGACATTAAACAGCTTCCAGAGAGTGTGG 2133
QY 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639
Db 2134 CTTCAGATTAAACAGAACCTGAGACTTGATGCACTTCTTCTGCGCTCCAGCACTGTCCG 2193
QY 640 TyrLeuArgLysIleArgValAspValLysGlyTyrPheProArgAspGluSerAlaGlu 659
Db 2194 TATTGGGGAATAATTCCGGTGTGATGTCAAGAGGATCTTCCCAAGAGATGATGCTCGTAG 2253
QY 660 AlaCysProValValProLeuTyrPheArgAspLysThrLeuIleGluGluGlnTyrGlu 679
Db 2254 GCATGTCCTGTGTCTCTTATGATGAGGAGATTAAGACCTTCATGAGAGAGAGTGGAA 2313
QY 680 AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSer 699
Db 2314 GATTTCGTCTCCATGCTGTGGCACCCACCACTGGGAGAGCTGGAGAGAGAGC 2373
QY 700 IleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLys 719
Db 2374 ATCCTGACAGAGCGGCGCATGAAGACCTGTGTGCCAAGCTGAGGCAATCCACCTGCAAG 2433
QY 720 IleGluThrLeuMetPheArgAsnAlaGlnIleThrProGlyValAlaGlnHisLeuTyrArg 739
Db 2434 ATTCAGAGCCCTGATGTTTAAGAAATGACAGATTAACCTGTGTGCAACCTTGTGAGA 2493
QY 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyTyrThrHisLeuLysGlu 759
Db 2494 ATGTCATGGCCAAACCGTAACTTAAGATCCCTCAACTGGAGAGCAACCACTGAAGAA 2553
QY 760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779
Db 2554 GAGAGTGAAGATGGGTGTGAGGCTTGAAGCTTAAACACCCAAAGTGTGTGGAGTCTTTG 2613
QY 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
Db 2614 AGGCTGATGTGCTGTGATTTGACCATGCTGTGTTACTGTAAGATCTTCCAAATCTTTAG 2673
QY 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
Db 2674 ACCTCCCCAGCGCTGAATCTCTGAGGCTGTGCAGAGAAACAAAGGTGACAGACGAGGTA 2733
QY 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
Db 2734 ACCGCTCTCAGTATGCTTGAAGGGTCTCCAGTGGCGCCTTGCAAGAGCTGATATGAGAG 2793
QY 840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db 2794 GACTGTGACATCAAGCAAGCGGTTGCGAGAGTGTGCTTCAGGCTTGTGTCAAGCAACGG 2853
QY 860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
Db 2854 AGCTTGACACACTGTGTCTATCAATCAACACAGCTGGGAGAACGAGTGAATCTACTG 2913
QY 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db 2914 TGTGCATCCATGAGGCTTCCCACTGATGTCTCAAGAGGTGTATGCTGAATCAAGTGTGAC 2973
QY 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTyrPheThr 919
Db 2974 CTGAGACAGGCTGTGCTGTGTTCTTTGCACTTGGCTTATGGGTAACTATGCTAGC 3033
QY 920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlyVal 939
Db 3034 CACTGAGCTTATGACAAAGACCTGTGAGAGACAAATGAGCGTGAAGCTTCTGTGAGAGTCT 3093
QY 940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959

Db 3094 ATGAGAACCATCTTGCATCTCCAGGACCTGGAGTTGTAAGTGCATCTCACCGCC 3153
Qy 960 AIAcyecyegluSerLeuSerCyava111eserArgserArgh1sleuylsSerLeuasp 979
Db 3154 GCGGCTGTGTGAGTCTGTCTCTGTGTGTATCTCGAGAGCAGACCTGMAAGAGCTGTGAT 3213
Qy 980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCySGluGlyLeuylsGln 999
Db 3214 CTCACGACATGCGCTGGGTGACGAGTGGAGTGTCTGCTGCTGCGAGGAGCTAGAGCA 3273
Qy 1000 LysAsnSerValLeuThrArgLeuGlyLeuylsAlaCySGlyLeuThrSerAspCySg 1019
Db 3274 AAGAAAGTGTTCGACGAGACTCGGGTTGAAGGACATGGACCTTCGATTGCTGT 3333
Qy 1020 GluAlaLeuSerLeuAlaLeuSerCyAsnArgh1sleuThrSerLeuAsnLeuValGln 1039
Db 3334 GAGGACCTCTCCCTTGGCCCTTCTTCGCAACCGGACATCGACAGCTTAAACCTGGTGAG 3393
Qy 1040 AsnAsnHisSerProLySGlyMetMetLysLeuCySerAlaPheAlaCyProThrSer 1059
Db 3394 AATTACTTCAGTCCCAAGAGATATGAGCTGTGTCTGCTTGGCTTCCCAAGCTCT 3453
Qy 1060 AsnLeuGlnle1eglyLeuThrLysTrpGlnTyProValGlnleArgLysLeuLeu 1079
Db 3454 AACTTACAGATTAATTTGGCTGTGGAATGGCAGTACCCTTGCAATAGAGAGCTGTG 3513
Qy 1080 GluGluValGlnLeuLeuLysProArgValAla11leapGlySerTrpHisSerPheasp 1099
Db 3514 GAGAGAGTGCAGCTACTCAACCCCGAGTCTGTAATGACGGTAGTGGCAATCTTTTGAT 3573
Qy 1100 GluAspAspArgHis 1104
Db 3574 GAAGATGACCGGTAC 3588
RESULT 8
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAEL
; APPLICANT: BECKMANN, GREGG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216, 645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-645-3
Alignment Scores:
Pred. No.: 0 Length: 3830
Score: 5683.50 Matches: 1087
Percent Similarity: 95.87% Conservative: 5
Best Local Similarity: 95.43% Mismatches: 12
Query Match: 80.34% Indels: 35
DB: 6 Gaps: 2
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Qy 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysSerSerSerGluSer 40

Db 61 CTAGACAAAGAGAAATTCAGACATTCAGAGAAATTAAGAGAAATCTTCAGAAATCG 120
Qy 41 ThrThrCysSerL1eProGlnPheGlu11egluAsnAlaAsnValGluCyLeuAlaLeu 60
Db 121 ACCAGATGCTTATTCACAGTTTGAATTCAGAAATTCAGAGATGCTGCAATGCTGGCATC 180
Qy 61 LeuLeuH1sGluTyTrpGlyAlaSerLeuAlaTrpAlaThrSerL1eSerL1ePheGlu 80
Db 181 CTCTTCGATAGATTTATGAGATCCCTGGCTGGGCTAGTCCATTAGCATCTTTGAA 240
Qy 81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysL1eSerGln 100
Db 241 AACATGAACCTGCGAACCTCTCGAGAGAGCAGGGATGACATGAAAAATTCACAGAA 300
Qy 101 -----AlaMetGluGlnGluGlyAlaThrAla11leArgLysGlnGln--- 115
Db 301 GATCCTGAAGCAAGATGACATGACAAAGACCAAGAAAGAAAGTCCGAAAAATTA 360
Qy 115 ----- 115
Db 361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTGACTGCAATATTAACAC 420
Qy 116 -----GluL1eSerGlnAlaMetGluGlnGluGly 125
Db 421 AAGTATGTTGGAATTCATCTTCTTTGCAAGAAATTCACAAAGTATGGAACAAAGAGT 480
Qy 126 AlaThrAla11leArgLysGlnGluGlnGlyLysGlyGlyAspTrpTrpAspTyLysSer 145
Db 481 GCCACAGAGAGAGACAGAAAGAAACAGACATGAGGTGACACATGAGGACTTACAGAGT 540
Qy 146 HisValMetThrLysPheAlaGluGluLysAspValArgArgSerPheGluAsnThrAla 165
Db 541 CACGTGATGACCAATTCGCTGAGAGAGAGATGATGCTGATTGTTGAAACACATGCT 600
Qy 166 AlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPhe 185
Db 601 GCTGACTGGCCGGAATGCAAACTGGCTGTGTCTTTGATTCAAGCCGTGGGGCTTC 660
Qy 186 ArgProArgThrVal11leuH1sGlyLysSerGlyL1eGlyLysSerAlaLeuAlaArg 205
Db 661 CGGCTTCGACGGGTGTCTGACGAAAGTCAAGAAATGGAAATCGGCTTACCGCA 720
Qy 206 ArgL1eValLeuCySTrPAlaGlnGlyGlyLeuTyTrpGlnTyMetPheSerTyValPhe 225
Db 721 AGGATCGTGTGTGTGTGGCCCAAGTGCATCTACAGGAAATGTTCTCTAGCTTTC 780
Qy 226 PheLeuProValArgGluMetGlnArgLysGlyLysSerSerValThrGluPheL1eSer 245
Db 781 TTCCTCCCGTTAAGAGATGACGCGGAAGAGAGACATGTCACAGATTCATCTCC 840
Qy 246 ArgGluTrpProAspSerGlnAlaProValThrGluL1eMetSerArgProGluArgLeu 265
Db 841 AGGAGTGGCCAGACTCCAGAGCTCCGGTGAAGAGATCAATGTCCTCGAACGAAAGGCTG 900
Qy 266 LeuPheL1eL1eAspGlyPheAspAspLeuGlySerValLeuAsnAspAspThrLysLeu 285
Db 901 TTGTTTCATTTGACGGTGTTCGATGACCTGGGCTGTCTCTCAACAAGACAAAGCTC 960
Qy 286 CysLysAspTrpAlaGluLysGlnProPheThrLeuL1eArgSerLeuLeuArgLys 305
Db 961 TGCAAAAGCTGGGCTGAGAAACAGGCTCGTTTCAACCTCATACGACATCTGTGAGAG 1020
Qy 306 ValLeuLeuProGluSerPheLeuL1eVal11ThrValArgAspValGlyThrGluLysLeu 325
Db 1021 GTCTGTCTCCCTGAGTCTTCTTATCTGTCACCGTCAGACAGCTGGGCAAGAGAGCTC 1080
Qy 326 LysSerGluValAlaSerProArgTyTrpLeuLeuValArgGlyL1eSerGlyGluGlnArg 345
Db 1081 AAGTCAGAGCTGTGTCTCCCGTTACCTGTTAGTAAAGAAATTCGGGGAAACAAAGA 1140
Qy 346 L1eHisLeuLeuGluArgGlyL1eGlyGlnH1sGlnTySerThrGlnGlyLeuArgAla 365

Dh 1141 ATCCACTGCTCCTTGAGCGCGGATTGTGAGCATCAGAAAGACACAGGGTTGCGTCCG 1200
Qy 366 TlMeCAspAaSpAaRgGlUleuLeuAaSpGlnCySglInValProAlaValGlySerLeuIle 385
Db 1201 ATCATGAACAACGCTGAGCTGCTGACACAGTGCAGGATGCCGCGGAGCTCTTCATC 1260
Qy 386 CySValAlaLeuGlnLeuGlnAaPValValGlyGlySerValAlaProPheAsnGlnThr 405
Db 1261 TGGGTGGCCCTGGACGTGACAGAGCTGTGGGGAGAGCGTCCGCCCTTCAACCAAAACG 1320
Qy 406 LeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProAlaGlyValValArg 425
Db 1321 CTCACAGGCTGTGACCGCGCTTTGTGTTCATCATGCTCACCCCTCAGAGCGTGTCCGG 1380
Qy 426 ArgCySLeuAaSnLeuGlnGlnArgValValLeuHisArgPheCySArgMetAlaValGln 445
Db 1381 CGCTGCTCATCTGAGAGAAAGATTGTCTTGAAAGGCTTTCGCCATAGCTGTGGAG 1440
Qy 446 GlyValTTPAaAaRgLySerValPheAaPGLyAaPheAaPheMetValGlnGlyLeuGly 465
Db 1441 GGAAGTGAATAGAAAGTCAAGTGTTCAGCGTGCACACCTCATGTTCAAGGACTCGGG 1500
Qy 466 GluSerGlnLeuAaRgAlaLeuPheHisMetAaSnIleLeuLeuProAaPheSerHisCySGLn 485
Db 1501 GAGTCTGAGCTCCGTGCTCTGTTTCATGAAACATCCTTCTCCAGACAGCCACTGTAG 1560
Qy 486 GluTyrTyrThrPhePheHisIleLeuSerLeuGlnAaPheCySAlaAlaLeuTyrTyrVal 505
Db 1561 GAGTACTACACTTCTTCCACTCAGTCTCAGAGACTTCTGTGCCGCTGTACTACGTG 1620
Qy 506 LeuGlnGlyLeuGlnIleGlnProAlaLeuCySProLeuTyrValGlnTyrThrLyArg 525
Db 1621 TTGAAGGCGCTGGAATCGAGCCAGCTCTCGCCCTCTGATCGTTGAGAAACAAAGAGG 1680
Qy 526 SerMetGlnLeuLySerGlnAlaGlyPheHisIleHisSerLeuThrPheLyArgPheLeu 545
Db 1681 TCCATGAGAGCTTAAACAGGAGGCTCTCATATCCACTCGCTTGTGATGAAGCGTTTCTTG 1740
Qy 546 PheGlnYLeuValSerGlnAaPValArgArgProLeuGlnValLeuLeuGlnCySProVal 565
Db 1741 TTGGCTCTGTAACGAAAGCTTAAGAGGCCACTGAGAGTCTCTGCTGGGCTGTCCGTT 1800
Qy 566 ProLeuGlnYValLySerGlnLySerLeuHisIleTyrValSerLeuLeuGlnGlnProAaSn 585
Db 1801 CCCCTGGGGGTGAAGCAGAAAGCTTCTGCACTGGGCTCTCTGTTGGGTCAAGCACTTAAT 1860
Qy 586 AlaThrThrProGlyAaPThrThrLeuAaPAlaPheHisIleCySLeuPheGlnThrGlnAaPLeu 605
Db 1861 GCCACCAACCCCAAGAGACACCTGTGAGCGCTTCCACTGTTTCGAGACTCAAGACAA 1920
Qy 606 GluPheValArgLeuAlaLeuAaSerPheGlnGlnValTyrLeuProIleAsnGlnAaSn 625
Db 1921 GAGTTTTCGCTTGGCATTTAAACAGCTTCCAAAGATGTGGCTTCCGATTTAAACAAG 1980
Qy 626 LeuAaPLeuIleAlaSerSerPheCySLeuGlnHisIleCySProTyrLeuAaRgLyIleArg 645
Db 1981 CTGGACTGTGATAGCATCTTCTCTTCTGCTCCAGCACTGCTCGATTTGGCGAAATTCGG 2040
Qy 646 ValAaPValLySerGlyIlePheProArgAaPGLySerAlaGlnAlaCySProValValPro 665
Db 2041 GTGATGTCAAAAGGATCTTCCCAAGAGATGAGTCCGCTGAGGATGTCTGTGTCTCT 2100
Qy 666 LeuThrPheArgAaPLeuThrLeuIleGlnGlnGlnThrGlnAaPheCySLeuMetLeu 685
Db 2101 CTATGAGAGCGGATTAAGCCCTCATTTGAGAGAGAGTGGAGAAATTTCTGTCTCATGCTT 2160
Qy 686 GlyThrHisProHisIleLeuArgGlnLeuAaPLeuGlySerSerIleLeuThrGlnArgAla 705
Db 2161 GGACCAACCAACCAACCTGCGGCACTGGAGCTGGGAGAGCATCTGACAGACGGGACC 2220
Qy 706 MetLyThrLeuCySAlaLySerLeuArgHisProThrCySlySIIleGlnThrLeuMetPhe 725
Db 2221 ATGAAGACCCGTGTGTGCAAGCTGAGGATCTCCACTGCAAGATACAGAACCTGATGTTT 2280

Qy 726 ArgAaSnAlaGlnIleThrProGlyValGlnHisIleuTyrArgIleValMetAlaAaSnArg 745
Db 2281 AGAAATGCAAGATTACCCCTGTGTGCAAGCACTCTGAGAAATCGTCAATGCCCAACGT 2340
Qy 746 AsnLeuArgSerLeuAaSnLeuGlyGlyThrHisIleuLySerGlnAaPValArgMetAla 765
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Qy 786 LeuThrHisAlaCySlyLeuLySIIleSerGlnIleLeuThrThrSerProSerLeuLyS 805
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Db 2581 TTGAAGATCTCCAGATGCGCCTGACAGACTGATCTGAGAGACTGTGGCATTCACAGCC 2640
Qy 846 ThrGlyCySGLnSerLeuAlaSerAlaLeuValSerAaAaRgSerLeuThrHisIleuCyS 865
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Qy 866 LeuSerAaAaAaSerLeuGlyAaSnGlnGlyValAaSnLeuLeuCySArgSerMetArgLeu 885
Db 2701 CTATCCAAACAAAGCTCGGGGAAACGAAGTGAATCTACGTGTGATCCATCAGAGCTT 2760
Qy 886 ProHisCySLeuSerLeuGlnArgLeuMetLeuAaSnGlnCySHisIleuAaPThrAlaGlyCyS 905
Db 2761 CCCACTGTGTGCTTGCAGAGGCTGATGCTGAATCAGGCCACTGACAGCGCTGTGT 2820
Qy 906 GlyPheLeuAlaLeuAlaLeuMetGlyAaSnSerTyrLeuThrHisIleuSerLeuSerMet 925
Db 2821 GGTTTTCTTCACTTGGCTTATGAGTACTCACTAGCTGACGCACTGAACTTAAAGCATG 2880
Qy 926 AsnProValGlnAaPAnGlyValLySLeuLeuCySGLnValMetAaRgLyProSerCyS 945
Db 2881 AACCTGTGAAAGACAATGGCGTGAACCTTGTGCGAGGTCTGAAGAAACAATCTTGT 2940
Qy 946 HisLeuGlnAaPLeuGlnLeuValLySLeuHisIleuThrAlaAlaCySGLySerLeu 965
Db 2941 CATCTCAAGACCTGAGATGTGTAAAGTCAATCTCACCCCGGTGCTGTGAAGACTG 3000
Qy 966 SerCySValIleSerArgSerArgHisIleuLySerLeuAaPLeuThrAaPAnAlaLeu 985
Db 3001 TCCGTGTGATCTCGAAGACACAGACACTGAAGCCTGTGATCTCAAGCAATGCCCTG 3060
Qy 986 GlyAaPGLyGlyValAlaAlaAlaLeuCySGLnGlyLeuLySGLnLySLeuSerValLeuThr 1005
Db 3061 GGTGACGCTGGGTGTGTGTGACTGTGAGAGGACTGAAGCAAAAGAAAGATGTCTGACG 3120
Qy 1006 ArgLeuGlyLeuLySAlaCySGLyLeuThrSerAaPLeuCySGLnAlaLeuSerLeuAla 1025
Db 3121 AGACTCGGGTTGAAGGATGTGACTGACTTTCATGTTGCTGTAGGCACTTCTTGGCC 3180
Qy 1026 LeuSerCySAlaAaRgHisIleuThrSerLeuAaSnLeuValGlnAaAaPheSerProLyS 1045
Db 3181 CTTTCTGCAACCGGCATCTGACACAGTCTAAACCTGTGTGAGAAATTAATCAATGCCAAA 3240
Qy 1046 GlyMetLeuLySLeuCySLeuAlaPheAlaCySProThrThrSerLeuGlnIleIleGly 1065
Db 3241 GGAATGATGAAGCTGTGTGTGGCTTGTGCTGTCCAGCTTAACTTAAGATTAATTTGGG 3300
Qy 1066 LeuThrLySerTyrPGLnTyrProValGlnIleArgGlyLeuLeuGlnGlnValGlnLeuLeu 1085
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Db      3361  AACCCGAGTCGTAAATTGACGATGTTGGCATCTTTTATGATGAATGACCGGTAC 3417
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RESULT 9
US-10-092-900A-347
: Sequence 347, Application US/10092900A
: Publication No. US20040043382A1
: GENERAL INFORMATION:
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Sptyek, Kimberly A.
: APPLICANT: Shenoy, Suresh G.
: APPLICANT: Taubler Jr., Raymond J.
: APPLICANT: Pena, Carol E.A.
: APPLICANT: Li, Li
: APPLICANT: Zeehuseen, Bryan D.
: APPLICANT: Gusev, Vladimir Y.
: APPLICANT: Ji, Weizhen
: APPLICANT: Gorman, Linda
: APPLICANT: Miller, Charles E.
: APPLICANT: Kekuda, Rameen
: APPLICANT: Paturajan, Meera
: APPLICANT: Gangolli, Bsha A.M.
: APPLICANT: Vernet, Corine A.M.
: APPLICANT: Guo, Xiaojia Saeba T.
: APPLICANT: Tchernev, Velizar T.
: APPLICANT: Fernandes, Elma R.
: APPLICANT: Caeman, Stacie J.
: APPLICANT: Malyankar, Uriel M.
: APPLICANT: Gerlach, Valerie
: APPLICANT: Liu, Yi
: APPLICANT: Anderson, David W.
: APPLICANT: Spaderna, Steven K.
: APPLICANT: Catterton, Elina
: APPLICANT: Leite, Mario W.
: APPLICANT: Zhong, Haihong
: APPLICANT: Alsobrook, John P.
: APPLICANT: Lepley, Denise M.
: APPLICANT: Rieger, Daniel K.
: APPLICANT: Burgess, Catherine E.
: TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 21402-290C
: CURRENT APPLICATION NUMBER: US/10/092,900A
: CURRENT FILING DATE: 2002-03-07
: PRIOR APPLICATION NUMBER: USN 60/274,322
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: USN 60/283,675
: PRIOR FILING DATE: 2001-04-13
: PRIOR APPLICATION NUMBER: USN 60/338,092
: PRIOR FILING DATE: 2001-12-03
: PRIOR APPLICATION NUMBER: USN 60/274,281
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: USN 60/274,191
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: USN 60/325,681
: PRIOR FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: USN 60/304,354
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: USN 60/279,995
: PRIOR FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: USN 60/294,899
: PRIOR FILING DATE: 2001-05-31
: PRIOR APPLICATION NUMBER: USN 60/287,424
: PRIOR FILING DATE: 2001-04-30
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 768
: SEQ ID NO 347
: LENGTH: 3226
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (69)..(3168)

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US-10-092-900A-347			
Alignment Scores:			
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Score:	5120.00	Matches:	977
Percent Similarity:	96.95%	Conservative:	7
Best Local Similarity:	96.26%	Mismatches:	20
Query Match:	72.38%	Indels:	11
DB:	7	Gaps:	1
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QY	121	MetguglugluglYAlaThra1aa1agiutrglugluglgn-gly-----	135
DB	173	CAGCCTCAAGTGCAGAGCTCCCTTCACAGAACAGAGCGCTCGGGCCGCCACCTGGG	232
QY	136	-----H1eglyYAspPhr1rpaaprytlyYserH1eVaimetHrly	150
DB	223	CTCAGAGCTTGGGCTGCATGAGAGTACACATGAGACTCAAGAGTCACTGATGACCA	292
QY	150	aphea1agiugluglYaaPva1AArgSerPhegluaantHra1aa1aaspTrrProgl	170
DB	293	ATTCCCTGAGAGAGAGATGACGTGCGTAAACATCTGCTGACCTGAGCTGGCGGA	352
QY	170	uMetglnThrleua1aglyAlaPheaSpserAphaTrrg1YpheaArgProaTgThra	190
DB	353	AATGCAACGTTGGCTGGTGTGTTGATTCAACAGCGTGGGCTTCGGCTTCGACGGGT	412
QY	190	lYal1euh1eglyYsergly11eglyYseralaleua1aaTgArg11eVal1eucy	210
DB	413	CGTTCGCAACGAAAGTCAGAAATGGGAAATCGGCTCAGACAGAAAGATGCTGTG	472
QY	210	sTrrpa1aglnglyYleuYtrglnG1wmetPseserYra1PhePheLeuProValAr	230
DB	473	CTGGGGGCAAGGTGAGCTTACAGAGAAATGTTCTTCTACGTCTTCTCCCGCTTAg	532
QY	230	ggluMetglnAArg1Yslyg1uSerSerVal1Thrg1uPhe11eserArg1uTrrProa	250
DB	533	AGAGATGACAGCGGAGAGAGAGAGAGAGTGTCAACAGTTCACTCCAGGAGTGGCCAG	592
QY	250	pSerGlnAlaProVal1Thrg1u11eMetSerAArgProgluAgluLeuPhe11e11eas	270
DB	593	CTCCAGAGGCTCCGGTGACCGAGATCATGTCCGACAGAAAGGCTGTGTCTCATTTGA	652
QY	270	pGlyPheAraPleuuglyYserVal1leuamamAraPrrlyYleuCYslyAAspTrrAl	290
DB	653	CGGTTTCAGTGAACCTGGGCTGTGTCTCTCAACATGACACAAAGCTTCGCAAGACTGGGC	712
QY	290	agluYsGlnProPheThrleu11eArgSerleuAArg1YsVal1leuLeuProgl	310
DB	713	TAGAGAGAGAGCTCCGTTACCTCATAGAGTGTGCTGAGGAAGTCTGCTCCCTGA	772
QY	310	uSerPheLeu11eVal1Thra1ArgAraPval1Thrg1u1YsleuYsGlnVal1Ya	330
DB	773	GTCTTCCTCGATCGTACCGTCAGAGACGTGGGACACAGAAAGCTCAAGTCAAGGTCTGT	832
QY	330	1serProAArg1YrleuLeuVal1Arg1Y11eserglyYglnArg11H1sleuLeu	350
DB	833	GTCTCCCTCCCTTACCTGTGTTAGAGAAATCTCCGGGAAACAAAGAAATCCATGTGCTCT	892
QY	350	uGluAArg1Y11eglyYglnH1sGlnYerThrglnglyYleuAArgal1eMetAAspAra	370
DB	893	TAGAGCGGGGATTTGGTGAAGTCAAGAGACACAGAGGTTGCGTGCATATGAACAACG	952
QY	370	gGluLeuLeuAraPginCYsGlnVal1Proa1Val1GlySerLeu11eCYsVal1AlaLeuG1	390
DB	953	TGAGGCTGCTGACAGTGCAGAGTGGCCCGCGGGGCTCTCTCATCTGCGTGGCTGCA	1012
QY	390	nLeuGlnAraPval1aglyYglnSerVal1AraProPheAraGlnThrLeuThrlYleuH1	410

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410 GAAIAAIApHeValPheHISglIeuThrProArgIValValArgArgCySleuAne 430
1073 CGCCGCTTGTGTTCATCAGCTCACCCCTCAGAGGGGTGGTCCGGGCTGTCAATCT 1132
430 uGIuGIaArgValValIleuIysArgPheCySArgMetAlaValGIuGIuValTTPaenAr 450
1133 GAGGAAAGAGTTGTCTGAAAGCCCTTCTGCGTATGGCTGTGAGGAGATGTGGATAG 1192
450 gIySerValPheAapGIyAapApleuMetValGIuGIyIleuGIyGIuSerGIuIleuAr 470
1193 GAAGTCAGTGTGTGACGGTGCACACCTCATGTGTCAAGACATCGGGAGCTGAGCTCCG 1252
470 gAlaIeuPheHISemecAsnIleIeuIeuProAapSerHISCySglIuGIuIyTyrThrPh 490
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490 ePheHISleuSerIeuGIuAapPheCySAlaIeuTyrTyrValIleuGIuGIyIleuGI 510
1313 CTTCCACCTCATGTCTCAGAGATTTCTGTGCGCTTGTACTAGCTTTAGAGGCTCGCA 1372
510 uIIeGIuProAlaIeuCySapProIeuIyValGIuIySerThrIyAArgSerMetGIuIe 530
1373 AATCGAACCAAGCTCTGCGCTCTGTAGTTCAGAGAACAAAGAGCTCCATGAGACTTAA 1432
530 gGIuAlaGIyPheHISglIeISerIeuIyTyrMetIyAArgPheIeuHISglIyIleuValIse 550
1433 ACAGGCAAGGCTTCATATCCATCGCTTGTGATGAACGGTTCTGTGTGGCTCGAG 1492
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1493 CGAAAGCGTAAGAGAGGCCATCGAGAGCTCTGTGGGTGTCTCCCTCGGGGAGTAA 1552
570 gGIuIySleuIeuHISglIyValISerIeuIleuGIyGIuGIuProAsnAlaThrThrProGI 590
1553 GCAGAACCTTCTGCACTGGCTCTCTGTGGGTCAACAGCGTAAATCCACACCCAGG 1612
590 yAapThrIleuAapAlaPheHISCySleuPheGIuThrGIuAapIyArgIuPheValArgIe 610
1613 AGACACCCCTGACGCTTCCATGTCTTTCAGACCTCAAGACAAAGATTTGTCCCTT 1672
610 uAlaIeuAapSerPheGIuGIuValTyrIleuProIIaSngIInaSnIleuApleuIIeAl 630
1673 GGCATTAAAGACTTCCAGAGAGTGTGGCTTCCATTAAACAGAACCTGACATTGAAGC 1732
630 aSerSerPheCySleuGIuHISCySProIyTyrIleuArgIyIleArgValAapValIySGI 650
1733 ATCTTCTTCTGCTCCAGCACCTGTCCGTATTTCGGAATAATCGGGTGGATGCAAGG 1792
650 yIIePheProArgAapIuSerAlaGIuAlaCySProValValProIeuTyrMetAlaArg 670
1793 GATCTTCCCAAGATATAGTCCGCTGAGGCAATGTCTGTGTCTCTCTATAGAGCGGGA 1852
670 pIySerThrIleuIIeGIuGIuGIuTyrGIuAapPheCySermetIleuGIyThrHISProHIS 690
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710 gAlaIyIleuAargHISProHISCySIIeGIuThrIleuMetPheArgAsnAlaGIuII 730
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750 uAenIeuGIyGIyThrHISleuIySGIuGIuAapValArgMetAlaCySglIuAlaIleuIy 770

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790 sTyrIleuIySISerGIuIIeIeuThrThrSerProSerIleuIySerIleuSerIleuAl 810
2213 TTACCTGAATGATCTCCCAATCTCTAGACCTCCCAAGCTCCCAATCTCTGAGCCCTGGC 2272
810 aGIyAenIyValThraSngIInIyAlaMetProIeuSerAapAlaIleuArgValISerGI 830
2273 AGGAAACAAAGTACAGACCAAGAGATGATCTCTCAAGAGGCTTGAAGCTTCA 2332
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2333 GTGCGCTTCAGAGAGTGTACTGTGAGAGCTGTGGATACAGACCGGTTGCCAGAG 2392
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890 uGIuArgIleuMetIleuAapGIuIyHISleuAapThrAlaGIyCySglIyPheIleuAlaIe 910
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1090 IIIeAapGIySerTyrHISerPheAapGIuAapAapArgHIS 1104
3113 AATGACGTAAGTGTGATCTTTTGTATGAAGATGACCGGTAC 3155

RESULT 10
US-10-399-443-5
Sequence 5, Application US/10399443

Publication No. US20040028669A1
 GENERAL INFORMATION:
 APPLICANT: The Government of the United States of America, as Represented by the
 APPLICANT: Secretary, Department of Health & Human Services, The National Institute
 APPLICANT: Health
 APPLICANT: Nelson, Lawrence M.
 APPLICANT: Tong, Zhi-Bin
 APPLICANT: Nelson, Lawrence
 APPLICANT: Zhi-Bin, Tong
 TITLE OF INVENTION: Human Gene Critical to Fertility
 FILE REFERENCE: 4239-64785
 CURRENT APPLICATION NUMBER: US/10/399,443
 PRIOR FILING DATE: 2003-04-16
 PRIOR APPLICATION NUMBER: PCT/US01/10981
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 5
 LENGTH: 3447
 TYPE: DNA
 ORGANISM: Mus musculus
 US-10-399-443-5

Alignment Scores:
 Pred. No.: 1.37e-275 Length: 3447
 Score: 2688.00 Matches: 554
 Percent Similarity: 66.49% Conservative: 186
 Best Local Similarity: 49.78% Mismatches: 293
 Query Match: 38.00% Indels: 81
 Gaps: 11

US-10-066-521-6 (1-1344) x US-10-399-443-5 (1-3447)

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Db 242 ----- 242
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Db 360 AAAGACCAAGGACAGACAGACAGACATCAAGAACTTACAACTTAAGAGAAAGAAAT 419
Oy 116 GluIleSerGlnAlaMetGluGlnGluGluGluAlaThrAlaAlaGluThrGluGluGln 135
Db 420 GAAAGTACAGAGCA-----GATTAAGAT 443
Oy 136 HisGlyGlyAaPThrTrpAaPTrpLysSerHisValMetThrLysPheAlaGluGluGln 155
Db 444 AATGAGGTGACTTCAAGACTACAGAGCCCATGTGATGCTTAAGTTCAGACCAAGTGTG 503
Oy 156 AspValaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 175
Db 504 GATTAACAC-----TATGACAGCCCAAGAGTGAATTAATATGTCT 542
Oy 176 GlyAlaPheAaPThrAaPTrpGlyPheAaPTrpAaPTrpValValaLeuHlSegLys 195
  
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Oy 196 SerGlyIleGlyLysSerAlaLeuAlaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 215
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Oy 216 LeuTrpGlnGlyMetPheSerTrpValPhePheLeuProValaAaGluMetGlnAaAa 235
Db 663 CTCTTCCAAAATAG---TCTTTGTATCTTCTTCTGTTAGAAATTAAGTGACA 719
Oy 236 LysGluSerSerValThrGluPheIleSerAaGluTrpProAaPThrGlnAlaProVal 255
Db 720 GAGAAAGACAGATTGGACAGCTGATGCTTAAGAGAGTCCAGACTCTGAGACTTATAG 779
Oy 256 ThrGluMetSerAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 275
Db 780 ACAAGATCATGCTCCCAACAGAAAGATCTTGTGTCATAGAGTGGTTGAGATATAG 839
Oy 276 GlySerValLeu---AaAaAaAaPThrLysLeuCyLysAaPThrAlaGluLysGlnPro 294
Db 840 GACTGTCTCTCCAAACATGATGATATGACATATCCAGAGACTGGAAGAGTGAACAGCC 899
Oy 295 ProPheThrLeuIleAaAaSerLeuLeuAaAaAaAaAaAaAaAaAaAaAaAaAaAa 314
Db 900 ATATACATCTGATGATGACAGCTCTGAGAAAGCTCTTACCTCACTCTTCTCATC 959
Oy 315 ValThrValaAaAaPValaGlyThrGluLysLysSerGluValaIleSerProAaPTrp 334
Db 960 ATTACACCAAGAAACACAGGCTTGAAGAAATCTCAAGTAAAGTGTGTCTCCCTCAT 1019
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QY 573 LeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThr 592
Db 1731 CTCACACACTGGGCTCTCTGATAGCTCAGCAGAGTCAATGGCACACACCCAAATGGACACC 1790
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QY 852 AlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeu 871
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QY 1072 ProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValAlaIle 1091
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QY 1092 AspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db 3291 GATGCTGATTGTGATGCTAGTGAAGATGACCGAAAC 3329

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RESULT 11
US-10-677-943-5
; Sequence 5, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; represented by the Secretary of the Department of Health and
; Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3447
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-677-943-5

Alignment Scores:
Pred. No.: 1,37e-275 Length: 3447
Score: 2688.00 Matches: 554
Percent Similarity: 66.49% Conservative: 186
Best Local Similarity: 49.78% Mismatches: 293

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Db 3291 GATGTGATGTGTATGATGATGAAGATGACCGAAAC 3329
RESULT 12
US-10-399-443-1
Sequence 1, Application US/10399443
Publication No. US20040028669A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Health
APPLICANT: Nelson, Lawrence M.
APPLICANT: Tong, Zhi-Bin
APPLICANT: Nelson, Lawrence
APPLICANT: Zhi-Bin, Tong
TITLE OR INVENTION: Human Gene Critical to Fertility
FILE REFERENCE: 4239-64785
CURRENT APPLICATION NUMBER: US/10/399,443
CURRENT FILING DATE: 2003-04-16
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/US01/10981
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1157
TYPE: DNA
ORGANISM: Homo sapiens
US-10-399-443-1
Alignment Scores:
Pred. No.: 2,536-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
DB: 7 Gaps: 0
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Qy 272 PheAspAspLeuGlySerValIleLeuAsnAspThrLysLeuCysLysAspTrpAlaGlu 291
Db 61 TTCATGACCTGGGCTGTGCTTCAACAATGACCAAGAGCTGTGCATAAAGACTGGGCTGAG 120
Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSer 311
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Qy 312 PheLeuIleValThrValArgAspValGlyThrGlnLysLeuLysSerGlnValValSer 331
Db 181 TTCCTGATCGTCAACCGTCAAGAGAGTGGGCAAGAAAGCTCAAGTCAAGAGTCTGTCT 240
Qy 332 ProArgTrpLeuLeuValArgGlyLysSerGlyGlnGlnArgIleHisLeuLeuGln 351
Db 241 CCCGTTACCTGTTAAGTGAAGATCTCCGGGAAACAAAGAAATCCCTGCTCTTGAG 300
Qy 352 ArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAspArgGln 371
Db 301 CGCGGAGTGGTGTGACATCAAGAACACAAAGGTTGGCTGTGATCAAGAACACCGTGTG 360
Qy 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391

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Qy 412 A1aPheValPheHisGlnLeuThrProArgGlyVal1A1aArgArgCysLeuAsnLeuGlu 431
Db 481 GCTTTGTTGTTCAATCAGCTCAACCTCGAGCGGTGTCGCGGCTGTTCTCAATCTGGAG 540
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Qy 452 SerValPheArgGlyAspAspLeuMetVal1GlnGlyLeuGlyGluSerGlyLeuArgAla 471
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Qy 532 A1aGlyPheHisGlnLeuSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlu 551
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; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.: 2,536-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
DB: Gaps: 0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)
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Db 61 TTCATATGACCTGGGCTGTGTCTCTCAACATGACCAAAAGCTCTGCAAAAGACTGGGCTGAG 120
Qy 292 LysGlnProProPheThrLeu1a1aArgSerLeuLeuArgLysVal1LeuLeuProGlySer 311
Db 121 AAGCAGCTCCGTTCACTCATACGAGTCTGTGAGAAAGTCTCTGCTGAGTCC 180
Qy 312 PheLeu1a1aVal1ThrValArgAspVal1GlyThrGluLysLeuLysSerGlyVal1a1Ser 331
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Qy 432 GlnArgVal1Val1LeuLysArgPheCysArgMetAlaVal1GluGlyVal1TrpAsnArgLys 451
Db 541 GAAAGAGTTCCTCGAAGCGCTTCTGCGGTATGCTGTGAGGAGGTGTGAATAATGAGAG 600
Qy 452 SerValPheArgGlyAspAspLeuMetVal1GlnGlyLeuGlyGluSerGlyLeuArgAla 471
Db 601 TCAGTGTTCAGCGGTGAGCACTCATGTTCAAGGACTCGGGGAGTTCAGACTCGTGTCT 660
Qy 472 LeuPheHisMetAsn1LeuLeuProArgSerHisGlyGluGlyTrpThrPhePhe 491
Db 661 CTGTTTCAATGAAATCTCTTCTCCAGACAGCACTGTGAGAGTACTTACCTTCTTC 720
Qy 492 HisLeuSerLeuGlnAspPheCysAla1aLeuTrpVal1LeuGluGlyLeuGluLys 511
Db 721 CACCTCAGCTTCAGAGACTTCTGTGCGGCTTGTACTACGTCTTAAAGGCGCTGGAATC 780
Qy 512 GlnProAlaLeuCysProLeuTrpVal1GlyTrpVal1ArgSerMetGlyLeuLysGln 531

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Db      781  GAGCGAGCTCTGCCCTCTGTAGTGAAGAGCAAGAGGCTTCATGAGCTTAACAG 840
Qy      532  AAGGlyPhehi8Ilehi8SerleuTPMeIyArPheleuPheglYleuValSerGlu 551
Db      841  GCGAGGCTTCATATCCACCTGCTTGATGAAGGTTTCTGTTGGCTCGGAGGAA 900
Qy      552  AspValArgArpProleuGluValleuLeuGlyCyseProValProleuGlyVallyeGln 571
Db      901  GAGGTAAAGAGGCCACCTGAGAGCTCTGCTGGCTGCTCCCTCCCTGGGGGTGAACAG 960
Qy      572  lyeleuLeuhi8ItrPValSerleuLeuGlyGlnInProAnaIaThrProGlyAsp 591
Db      961  AAGCTTCGACATGGGTCTCTGTTGGTCAGCAGGCTTAATGCACACCCGAGAGAC 1020
Qy      592  ThrleuAnaIaPhehi8CyseleuPhegluThrGlnAspIySgluPheValArgleuAla 611
Db      1021  ACCCTGAGCGCTTCCACTGTCTTTCGAGACTCAAGACAAAGATTGTTCCGTTGGCA 1080
Qy      612  leuAnaSerPheGlnGluValITrPleuProIleAnaGlnleuAnaPheleuIleAlaSer 631
Db      1081  TTAAACAGCTTCCAAAGAGTGTGCTTCGATTACCAAGAACTGAGCTTGATAGCATCT 1140
Qy      632  SerPheCyseleuGln 636
Db      1141  TCCTTCGCTCCAG 1155

RESULT 14
US-10-794-342-2
; Sequence 2, Application US/10794342
; Publication No. US20040253615A1
; GENERAL INFORMATION:
; APPLICANT: Inohara, Naohiro
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: NOD Nucleic Acids and Polypeptides
; CURRENT REFERENCE: UM-08922
; CURRENT APPLICATION NUMBER: US/10/794,342
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-794-342-2

Alignment Scores:
Pred. No.:          9,56e-190      Length:      3521
Score:             1885.50         Matches:      422
Percent Similarity: 56.65%         Conservative: 208
Best Local Similarity: 37.95%      Mismatches:  443
Query Match:       26.65%          Indels:       39
DB:                8              Gaps:         13

US-10-066-521-6 (1-1344) x US-10-794-342-2 (1-3521)
Qy      2  GluGlyAspIySerleuThrPheSerSerTyGlyleuGlnTrpCyseIyrgIuLeu 21
Db      28  GATTCATCATCATCTTCTTCTTCCGATTTTGGGCTGCTATTCATTTGGAGAGACTA 87
Qy      22  AspIySgluGluPheGlnThrPheIySgluLeuLeuIySlySlySerSerGluSerThr 41
Db      88  AACAAAGAGAAATTAATAATCACTCAAG---TTATTCTTAAGAGGACCATGAACTGAG 144
Qy      42  ThrCyseSerIleProGlnPheGlnIleGluAnaIaAnaValGluCyseleuAlaLeuLeu 61
Db      145  CATGGCTGACACCCCTGAATGAAGTGAAGAGGCGGAGGAGCACTGGCCAATTGG 204
Qy      62  leuhi8IyrgIyrgIyAlaSerleuAlaItrPalaThrSerIleSerIlePheGluAsn 81
Db      205  ATGAAAGAAATTTATCCAGAGAGAAAGCCCTGAGGTGTCTCTCAAAATCTTTGGCAG 264
Qy      82  MetAnaIyrgThrleuSerGluIyAlaIrgAAspAspMetIySlySlySerGlnAla 101
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Db      265  ATGAACTGAAGGATGTGTGTGAGAGAGCAAGAAAGAGATCAATGTGGGCCCACT 324
Qy      102  MetGluGlnGluIyAlaThrAlaIaIaGluThrGluGlnGlnIleSerGlnAlaMet 121
Db      325  ATGAGACCAATATATGCAAGGCTGAGAGACCAAGAA----- 363
Qy      122  GluGlnGluIyAlaThrAlaIaIaGluThrGluGlnGlnIyhi8IySglYAspThrTrp 141
Db      364  GATCAGAGGACAGTGGCG----- 393
Qy      142  AspTrIySserhi8ValMetThrIyPheAlaGluGluAspValaIaIaGlySerPhe 161
Db      394  GAATACAGAAATGTAAAGAAATTTTGATCATCACTTGAGAC---AAGAAGTCTTGG 450
Qy      162  GluAnaThrAlaIaAspTrp-----ProGluMetGlnThrleuAla 175
Db      451  GCTGAAAGCCTGAAGATTTCATCATGCAATTCAGAGAAAGATGAACAACTGTGGAA 510
Qy      176  GlYAlaPheAspSerAsp--ArgTrpGlyPheArgProArgThrYAlaValleuhi8Gly 194
Db      511  CACTGTTCATGTGATGTGCAAACCGGTGCACAGCACAAGATCGTGTTCAGAGGA 570
Qy      195  lyeSerGlyTleGlylySserAlaIeuaIaIyrgIleValleuCystrPalaGlnGly 214
Db      571  GCTGCTGAGTGGGAAACCACTTGTAAGAAAGCAATGTTAATTTGGAGAGAGGC 630
Qy      215  GlyleuTrGlnGlyMetPheSerTyValPhePheleuProValArgGluMetGlnArg 234
Db      631  AGTCTTACAGCAGACAGCTTAAAGTATGTTTATTCATCAATGAGAGAAATTAACAG 690
Qy      235  lyeleuGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaPro 254
Db      691  CTGAAGAGAGAGACTTGTGCTCAATGATCAAGAGACTGCGCCAGCAAGAGGCCCC 750
Qy      255  ValThrGluIleMetSerArgProGluArgleuLeuPheIleIleAspGlyPheAsp 274
Db      751  ATTGAAGAAATCAATGACAGCCAGAGTACCTCTGTTATTTATGACAGTTTCAGTGA 810
Qy      275  leuGlySerValleuAnaen---AspThrIySleCyseIySAspTrPalaGluIyGln 293
Db      811  CTGAACCTTGCCTTGAAGAACTGAGATTGCACGTGTGCAGAAAGCTGCACCAAGAAC 870
Qy      294  ProPheThrIleuIleArgSerleuLeuArgIyValleuLeuProGluSerPheleu 313
Db      871  CCAGTGCTTCCATCAAGATGTTTCTGAGAAAGTGAATGCTCCCTGAGGACATCCTTA 930
Qy      314  IleValThrValArgAspValGlyThrGluIySgluLeuIySserGluValIleSerProArg 333
Db      931  TTGGTGCACAAAGACTCACACTCTTAAGAGACTTAAGAGAGTTGTAAGAAATCACCAT 990
Qy      334  TyrleuLeuValArgGlyIleSerGlyGluGlnArgIlehi8leuLeuGluArgGly 353
Db      991  TATGTAGACTTACTAGGAATGTCTGAGAGATGCAGAGAGAGATATATTACAGTTT 1050
Qy      354  IleGlyIuhi8GluIySerThrGlnGlyleuArgAlaIleMetAnaAnaIyGluLeu 373
Db      1051  GAAGATTAAGAGTGGGCGCATGAAGATATCATGATCAATAAAGCAATGATGATCTGTT 1110
Qy      374  AspGlnCyseGlnValProAlaValGlySerleuIleCyseValAlaIeGlnleuGlnAsp 393
Db      1111  AGCATGTCCAAGTCCCTCAATGTGTGGCGCGCTTGATCTGTGTAAGCAGCAATATG 1170
Qy      394  ValIaGlyIySerValaIaProPheAnaGlnIleThrleuThrGlyleuhi8AlaIaPhe 413
Db      1171  GAGAGGCTGTATGTCAATGACCTGCGCAACACACAGCTGCTTTACTGCTAT 1230
Qy      414  ValPhehi8GlnleuThrProArgGlyValaIaIyrgIyCyseleuAnaIyGluIyArg 433
Db      1231  ATTTCATGCTTGTTCACACCA-----GTAGATGAGGCTCTCTCAATCAACCAACCA 1284
Qy      434  ValValleuIySArgPheCySArgMetAlaValGluGlyValITrPAnaIyIySerVal 453
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Db 1285 GCCCAGCTGAGAGACTGTCGCCAAGTCGCTCCCAAGGAAATATGACTATGACTTACCTG 1344
 Qy 454 PheAepGlyAspAepMetValGlnGlyLeuGlyGlnSerGlnLeuArgAlaLeuPhe 473
 Db 1345 TTTTACAGAGAAATCTCAGAAAGCTTGGTTACTGATCTGATGCTCTGATTTATG 1404
 Qy 474 HisMetAniLeuLeuProAepSerHisCysGlnGlnGlyTyrTyrPhePheHisLeu 493
 Db 1405 GACAGCAATATTTATTCAGAGAGCCAGATATGAAAAGCTGATGCTTACCCACTT 1464
 Qy 494 SerLeuGlnAepPheCysAlaAlaLeuTyrTyrValLeuGlnGly--LeuGlnLeu 512
 Db 1465 CATGTTCAAGAGTTTGTTCAGCTATGTTCTATATGTTGAAAGGAGTGGAGCTGG 1524
 Qy 513 ProAlaLeuCysProLeuTyr-----ValGlnGlySerHisArgSerMetGlnLeu 530
 Db 1525 AACCTTCCTCCAGCCTTTGAAAGATTGAACTTACCTTCAAGCAAGATTATATA 1584
 Qy 531 GlnAlaGlyPheHisIleHisSerLeuTyrMetLysArgPheLeuPheGlyLeuValSer 550
 Db 1585 GACCC-----CATTTGACACAGATGAAAGCTTTTCTTGGCTTTGAT 1632
 Qy 551 GluAspValArgArgProLeuGlnValLeuLeuGlyCysProValProLeuGlyValLys 570
 Db 1633 GAAGATCGAGTAAACACTGAGAGGACTTTTAACTGTAAATGTCACTGAAGATAAA 1692
 Qy 571 GlnLysLeuLeuHisLeuTyrValSerLeuLeuGlnGlnGlnProAlaAlaThrThrProLys 590
 Db 1693 TCAAGATTACTTCAGAGTATGAAAGTATTTAGAAACAGTGAATATCTTCACACAGCTG 1752
 Qy 591 AspThrLeuAspAlaPheHisCysLeuPheGlnTyrGlnAspLysGlnPheValArgLeu 610
 Db 1753 GGATTTCTGAGCTTTTCACTGCTGTATGAGATCAAGATTAAGCCTTTATAGCCAG 1812
 Qy 611 AlaLeuAsnSerPheGlnGlnValTyrPheProIleAsnGlnAsnLeuAspLeuIleAla 630
 Db 1813 GCATAGAGATGTTTCCCAAGGTTCCCATTAATATTTGTGAGAAATATCATTTGCTGTA 1872
 Qy 631 SerSerPheCysLeuGlnHisCysProTyrLeuAlaGlySileArgValAspValLysGly 650
 Db 1873 TCTCTTCTCTGCTTAAACACGCGGTGTTGCGGACATTCAGGCTGTCTGTAAGCTG 1932
 Qy 651 IlePheProArgAspGlnSerAlaGlnLysCysProValValProLeuTyrMetArgAsp 670
 Db 1933 GTATTGAGAGAAATTTAAAAACAAGCTCCCA--ACTTAACACTTGGAGATGCTAT 1989
 Qy 671 LysThrLeuIleGlnGlnGlnTyrPheLysPheCysSerMetLeuGlyThrHisProHis 690
 Db 1990 CGC-----ATTACTCAGCTTGGCAGATCTCTGTTCTGCTTCATTAACAATGACAC 2043
 Qy 691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCys 710
 Db 2044 TTGAGAGATGAGCACTGTACCATAGCAACTTGTAAATATGACAGATGAAATCTGCAAT 2103
 Qy 711 AlaLysLeuAsnGlnProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIle 730
 Db 2104 CATGAACCTTAAGCACCACCACTGTAACTACAAAGCTACTGTGAAATTTATCACTTTC 2163
 Qy 731 ThrProGlyValGlnHisLeuTyrArgIleValMetAlaAsnArgAsnLeuArgSerLeu 750
 Db 2164 CCGATGATGTTGTCAGAGATATCTCTCTTGTGATTCATTAACAAGATCTGATGATCTT 2223
 Qy 751 AsnLeuGlyGlyThrHisLeuLysGlnGlnValAspValArgMetAlaCysGlnAlaLeuLys 770
 Db 2224 GACCTTAAGAGGAGATGATATAGGAGATATAGGATGAACTTGTGTGAGGCTTGA 2283
 Qy 771 HisProLysCysLeuLeuGlnSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCys 790
 Db 2284 CACCAAGAGTAAACTACAGACTCTCAGGCTGGAATCTTGAACCTTAACCTATTTGT 2343
 Qy 791 TyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAla 810
 Db 2344 TGTCTAAATATATCTTAAGCTCTCATCAGAACGAGCTGATATTTCTGAATCTGCA 2403

Qy 811 GlyAsnLysValThrArgGlnIleValMetProLeuSerAspAlaLeuArgValSerGln 830
 Db 2404 ACCAATATATCTGTGATGATGAGAGTGCAGCTTTTGTGTGAGGCTTAAAGATCAAAAG 2463
 Qy 831 CysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAlaThrGlyCysGlnSer 850
 Db 2464 TGTATCTAGAGACAGCTCTCTTGAAGAGCTGTGTCTCACAGAGGCTGGCTGTGAGAT 2523
 Qy 851 LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSer 870
 Db 2524 CTTCCTTGGCTTCATCAGCAATTAAGACTGACCATTTGCTTGGCAGACAAATTC 2583
 Qy 871 LeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu 890
 Db 2584 TTGGGTATGAGTGAAGTAAAGCTTATGATGATGATCCCTGCAACATGCAATGATCTGT 2643
 Qy 891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeu 910
 Db 2644 AAGAGCTTGTGAGGCTTGCATTTCACTTCACTTACAGTGAATATCTGCAACT 2703
 Qy 911 AlaLeuMetCysAsnSerTyrPheThrHisLeuSerLeuSerMetAsnProValGlnAsp 930
 Db 2704 TCTCTTACACACACAGAGCTTACGATCTGATCTGATGATCAACTGCTGACAGAC 2763
 Qy 931 AsnGlyValLysLeuLeuCysGlnValMetArgLysProSerCysHisLeuGlnAspLeu 950
 Db 2764 AATGAGAGAGCTTCTGTGTGATGATCTTTCGGATCCAGACTTATCTTCAGAGCTTG 2823
 Qy 951 GluLeuValLysCysHisLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSer 970
 Db 2824 GAATGATGAGGCTGTGTTCTCATTAAGCAAGTTGTCTGATCTGCTGTTATTTTG 2883
 Qy 971 ArgSerArgHisLeuLysSerLeuAspLeuThrAspAlaLeuGlyAspGlyVal 990
 Db 2884 AATAACCCAACTGAGAGGCTTGACCTTGGAACAAACGATTGACAGATGATGAGTG 2943
 Qy 991 AlaAlaLeuCysGlnGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLys 1010
 Db 2944 AAAATCTGTGTGATGCTTGAAGATTCACAACTGTAACATTCAGAGGCTGGGTGAA 1030
 Qy 1011 AlaCysGlyLeuThrSerAspCysCysGlnAlaLeuSerLeuAlaLeuSerCysAsnArg 1030
 Db 3004 TACTGTGTTGACATCTCTGCTGTCAGATCTCTCTGCTCTTATCTGCAACAA 1063
 Qy 1031 HisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeu 1050
 Db 3064 AGACTGATTAAGATGATCTGACACAGAAATCTTGAAGATATGAAAGATGTGAAGTTA 3123
 Qy 1051 CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTyrPheGln 1070
 Db 3124 TATTAAGCTTGAAGCTCTTGAAGTAACTTACAACTTCAAGCTTCAAGGCTGTGCAAGAGCA 3183
 Qy 1071 TyrProValGlnIleArgLysLeuLeuGlnGlnValAlaGlnLeuLysProArgValVal 1090
 Db 3184 TTTGATGAGAAAGCCCAAGACTGCTGTGAGCTGTGGAGATTAGCAATCAACCTTAATC 3243
 Qy 1091 IleAspGlySerTyrHisSerPheAspGlnAspAsp 1102
 Db 3244 ATTAAGCCAGATTGTAACTATCATTAATGAAGAAGAT 3279

RESULT 15
 US-10-124-498-23
 ; Sequence 23, Application US/10124498
 ; Publication No. US20030017983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; APPLICANT: Wang, Weiye
 ; APPLICANT: Blacher, Maria
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
 ; FILE REFERENCE: 0734-367001
 ; CURRENT APPLICATION NUMBER: US/10/124, 498


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Db      1681 TTAGGGAGCGGTGCAATCTTCAGGAGACAGGTGATTCCTTGCGGATATTTACTGTC 1740
Qy      600 PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTyr 619
Db      1741 TTTCAAAATGCGAGATCTCGCTTTGTGAAAGAGAGGAACTTCCTCAAGAGCTTAAC 1800
Qy      620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639
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Qy      640 TyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaIu 659
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Qy      660 AlaCysProValValProLeuTyrMetCysArgLysPheThrLeuIleGluGluGlnTyr 679
Db      1921 TCT-----ACGTGGATTAACGCTCATC-----TGTTGGCAT 1953
Qy      680 AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuLysSer 699
Db      1954 CACATCTGCTGTGCTCACACAGCGGACCTTCAGAGCTTCAGGTGACAGACAGC 2013
Qy      700 IleLeuThrGlnArgAlaMetLysThrLeuCysValAlaLysLeuArgHisProThrCys 719
Db      2014 ACCCTCAGCGAGTGACCTTTGTGACCTGTGTACAGCTGAGGCACTCCAGCTGTGC 2073
Qy      720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTyrArg 739
Db      2074 CTTCAGAAAGCTTGAAATTAATTAACCTTTCCTTTTCGCCAGAGTTCGTGCTCTTAG 2133
Qy      740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyLysIleThrHisLeuLysGlu 759
Db      2134 GTGCTCTTTATTCAGCCACAGACTGAATACCTGAGCTTCACCTTCACCAAACTCTGCT 2193
Qy      760 GluAspValArgMetAlaCysGluValLeuLysHisProLysCysLeuLeuGluSerLeu 779
Db      2194 GATGACATCAGGTCCCTGTGATGCTCTTGAACATCA----- 2232
Qy      780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
Db      2232 ----- 2232
Qy      800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
Db      2233 -----GAGGCAAC----- 2241
Qy      820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
Db      2242 -----GTCAAAAGCTAGCGCTGGTA 2262
Qy      840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db      2263 AATTGTCACTCTCACTCACTGATGTGTAAGTCTTGCTGCGCTTCAACCAACAAG 2322
Qy      860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
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Qy      880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db      2380 TGTGAAGCCCTGTGACGCCACAGACAGGATCTGTATACCTGATGTGGCTTTTGGCAC 2439
Qy      900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTyrLeuThr 919
Db      2440 CTCAAGCAGAGTGTGCGGAATACATCTGAAATGCTTCTCGTAACAAGAGCGTGGC 2499
Qy      920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939
Db      2500 TATCTAAGCCTTCAAGTCTCTGAAGAGCAAGAGCACTGAATACTCTGCGAGGCC 2559
Qy      940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959
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Qy      960 AlaCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979
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Qy      980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
Db      2680 ATTGGGTGCATTAATTCGAGATGTGGGTGTGACAGCTGTGTGTGGGCTTACCGCAT 2739
Qy      1000 LysAsnSerValLeuThrArgLeuGlyLeuLysValAlaCysGlyLeuThrSerAspCys 1019
Db      2740 ACGGATTCGCGCTTAAGATTTCTGGGTGAAGATGTGGTTAAGACGACCTGCTGT 2799
Qy      1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
Db      2800 AAGATCTCGGCTGTCTTCACTGACAGTAAGACCTGCAGCAGCTCAACTGACCTTG 2859
Qy      1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
Db      2860 AACACCTTGACACACAGAGGTGTGTGTACTGTGTAGAGGCCCTGAGACACCCAGAGTGT 2919
Qy      1060 AsnLeuGlnIleIleGlyLeuTyrTrpGlnTyrProValGlnIleArgLysLeuLeu 1079
Db      2920 GCCCTGAGGTGTCTCGGCTGAGAAATGATTTGTATGAGAAACCCAGGCACTTCTG 2979
Qy      1080 GluGluValGlnLeuLeuLysProArgValAlaIleAsp----- 1092
Db      2980 ACGGCTGAGAGAGAGAAATCTTAACCTGACATCAAGATGACTGTGACATCA 3039
Qy      1093 -----GlySerThrHisSerPheAspGluAspAspArgHisLys 1105
Db      3040 AGGGTAGAGATCTGATTGCGAGAACTCG----- 3069
Qy      1106 IleGlyLeuThrPheArgLeuProGluSerArgAlaTyrProCysAlaLeuLeuTyrGly 1125
Db      3070 ---GCTCTGACTCGAACAACCTGCAAGAGCAGGAGCTGGAGC---CGTTACTTACATGAC 3123
Qy      1126 MetAsnProGluGlnLysArgValSerLeu 1136
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Search completed: January 21, 2006, 12:58:26
Job time : 2447 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using ~~fixme_p2n.p2n~~ model

Run on: January 21, 2006, 05:40:31 ; Search time 520 Seconds
(without alignments)
4594.313 Million cell updates/sec

Title: US-10-066-521-6

Perfect score: 7074
Sequence: 1 MEGXSLTFFSYGLQWCLYE.....DDHSGVSLGAGLEGIVS 1344

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -OPMT=fastac -SUFFIX=p2n.rml -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=dbs -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US1006521 @CGN 1 1 342 @runat_20012006_145858_21069 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1434	20.3	2985	US-10-781-294-15	Sequence 15, Appl
2	1320.5	16.7	3108	US-10-781-294-23	Sequence 23, Appl
3	955	13.5	4287	US-09-996-617-5	Sequence 5, Appl
4	955	13.5	4422	US-09-388-221B-1	Sequence 1, Appl
5	955	13.5	5444	US-09-996-617-1	Sequence 1, Appl
6	949	13.4	4200	US-09-388-221B-3	Sequence 3, Appl
7	949	13.4	4332	US-09-388-221B-5	Sequence 5, Appl
8	948	13.4	4466	US-09-388-221B-11	Sequence 11, Appl
9	945.5	13.4	4556	US-09-388-221B-9	Sequence 9, Appl

10	911	12.9	4931	US-10-183-770A-1	Sequence 1, Appl
11	721	10.2	2844	US-10-781-294-17	Sequence 17, Appl
12	721	10.0	2524	US-10-781-294-58	Sequence 58, Appl
13	705	10.0	2524	US-10-781-294-63	Sequence 63, Appl
14	672.5	9.5	2068	US-10-104-047-19	Sequence 19, Appl
15	646	9.1	2046	US-10-781-294-19	Sequence 3, Appl
16	630.5	8.9	1374	US-08-795-395-3	Sequence 3, Appl
17	630.5	8.9	1374	US-08-795-395-1	Sequence 1, Appl
18	621	8.8	1371	US-08-910-731-1	Sequence 1, Appl
19	621	8.7	1371	US-08-910-731-7	Sequence 7, Appl
20	612	8.7	1371	US-08-910-731-5	Sequence 5, Appl
21	607.5	8.6	1386	US-10-028-347-1	Sequence 1, Appl
22	544.5	7.7	2689	US-10-028-347-5	Sequence 5, Appl
23	527	7.4	2763	US-10-028-347-5	Sequence 870, Appl
24	406	5.7	3156	US-09-799-451-870	Sequence 21, Appl
25	400.5	5.7	1515	US-10-781-294-21	Sequence 42, Appl
26	379.5	5.4	4141	US-09-207-359B-42	Sequence 42, Appl
27	379.5	5.4	4141	US-09-340-620A-42	Sequence 84, Appl
28	379.5	5.4	4141	US-09-865-364-42	Sequence 42, Appl
29	379.5	5.4	4141	US-09-728-721-42	Sequence 42, Appl
30	366	5.2	3123	US-10-002-974-58	Sequence 58, Appl
31	364	5.1	3123	US-10-002-974-53	Sequence 53, Appl
32	364	5.1	3123	US-10-002-974-66	Sequence 66, Appl
33	364	5.1	3123	US-10-002-974-84	Sequence 84, Appl
34	364	5.1	3123	US-09-949-002-101	Sequence 101, Appl
35	364	5.1	4485	US-09-949-016-3209	Sequence 3209, Appl
36	364	5.1	4485	US-10-014-269-1	Sequence 1, Appl
37	364	5.1	4485	US-10-002-974-1	Sequence 1, Appl
38	363	5.1	3123	US-10-002-974-64	Sequence 64, Appl
39	363	5.1	3123	US-10-002-974-68	Sequence 68, Appl
40	363	5.1	4384	US-09-949-002-238	Sequence 238, Appl
41	362	5.1	3123	US-10-002-974-56	Sequence 56, Appl
42	362	5.1	3123	US-10-002-974-60	Sequence 60, Appl
43	361	5.1	3123	US-10-002-974-62	Sequence 62, Appl
44	361	5.1	3123	US-10-002-974-86	Sequence 86, Appl
45	360	5.1	3123	US-10-002-974-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-10-781-294-15
; Sequence 15, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Ioredana
; APPLICANT: Arieta, Maria Bugenia
; APPLICANT: Stenlik, Christian
; TITLE OF INVENTION: PAD Domain-Containing Polypeptides,
; FILE REFERENCE: P-14 4816
; CURRENT APPLICATION NUMBER: US/10/781,294
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2985
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2985)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1857)

OTHER INFORMATION: n = A,T,C or G
US-10-781-294-15

Alignment Scores:

Pred. No.:	4,57e-134	Length:	2985
Score:	1434.00	Matches:	339
Percent Similarity:	49.27%	Conservative:	199
Best Local Similarity:	31.04%	Mismatches:	430
Query Match:	20.27%	Indels:	124
		Gaps:	12

US-10-066-521-6 (1-1344) x US-10-781-294-15 (1-2985)

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Qy PheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlyLeuAerPlyGluGluPheGlnThr 28
Db |TTCCTGATTTTGGCTTTATGTGCTATCTGAGAGAGCTCAAAAAGAGAGAGCTTCAAGAAA 75
Qy 29 PheLysGlyLeuLeuLysLysLysSerSerGluSerThrThrCysSerLleProGlnPhe 48
Db |TTTAAAGAACATCTCAAGCAAAATGACTTTCAGAGCTTGAACTCAAGCAGATTCCTGAGCT 135
Qy 49 GluLleGluSerAlaIleuValGluCysLeuAlaLeuLeuLeuLysGlyTyrTyrGlyAla 68
Db |GAGGTCAAAAAGAGATCCGGGAAAGAACTTCGAAACCTTGATCAAGCAGCTATGAAGAA 195
Qy 69 SerLeuAlaTrpAlaThrSerLleSerLlePheGluSerMetAanLeuAerGlyThrLeuSer 88
Db |CAACAGCTTGAACATTAACCTTAAAGATCTTCAAAAGATG----- 237
Qy 89 GlyLysAlaArgAerPheMetLysLysLleSerGlnAlaMetGluGlnGluGlyAlaThr 108
Db |GATAGAAAGATCTCTGATGAAAGCTCATGAGGAGAGAGAAACAGAA 282
Qy 109 AlaAlaGluThrGluGlnGlnGlnLleSerGlnAlaMetGluGlnGlnGlyAlaThrAla 128
Db |TACACAAAGACCTTACAGCTCAGCAAGCAAGAAATTCAAGCCG----- 327
Qy 129 AlaGluThrGluGlnGlnGlnLysLleGlyLysAerThrTrpAerTyrLysSerHisValMet 148
Db |-----TTATGCTCCAGCAAGCTGCTGACAGAG 354
Qy 149 ThrLysPheAlaGluGluGluAerPheValArgAerSerPheGluAerThrAlaAlaAerTrp 168
Db |ATTCACCTATATCTTGAAGAGAAAGTCAACCAAGAA----- 390
Qy 169 ProGluMetGlnThrLeuAlaGlyAlaPheAerSerAerAerGlyPheArgProArg 188
Db |---GAAATGTGACATTTTGGACCGCTTTTGTCTCCCAAGAACTGGGAAACAGCCAGCT 447
Qy 189 ThrValAlaLeuHisGlyLysSerGlyLleGlyLysSerAlaLeuAlaArgArgIleVal 208
Db |ACATGTATATTCAGAGACCAAGAGAAATTCGAAAGAAAGCAACATCCGATGAAAGCTAGTG 507
Qy 209 LeuCysTrpAlaGlnGlyLysLysLysSerGlnLysMetPheSerTyrValPhePheLeuPro 228
Db |ATGGCTGTGTGGCAACAAGATCTTTCGGATAGAGTTGCTGTGACAGCTTATTTCTGAC 567
Qy 229 ValArgLysMetGlnArgLysLysLysSerSerValThrGluPheLleSerArgGluTrp 248
Db |TGCGAAGAACTGAGGAGAGTTGCCGCCCAACGAGTTGTGACTTGATTTCCAGAGAGTGG 627
Qy 249 ProAerSerGlnAlaProValThrGluLleMetSerArgProGluArgLeuLeuPheLle 268
Db |CTTACCCCGCTGCTCTATTAACAGAGATCGTGTCTCAACCGAGAGAGCTTGTGCTC 687
Qy 269 IleAerPlyPheAerAerPheLysLysSerValLeuAerAan--AerThrLysLeuCysLys 287
Db |ATCACACAGCTTCGAAGAGCTGCAAGGCGGCTTGAAACCAACCCGAGTCCGTGTGTGCT 747
Qy 288 AspTrpAlaGlyLysGlnProProPheThrLeuLleAerSerLeuLeuAerGlyValLeu 307
Db |GACTTGATGAGAAACGGCGGCTGCAAGGTCTTCTGACAGATTTGCTGAGGAGAAAGATG 807

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Qy 308 LeuProGluSerPheLeuIleValThrValArgAerValGlyThrGluLysLeuLysSer 327
Db |CTCCGAGGAGGCTCCCTGCTCATCGCATCAAAACCGGTGTGCCCAAGAGAGCTCCGGAGAT 867
Qy 328 GluValValAerProArgTyrLeuLeuValArgGlyLleSerGlyGlnGlnArgIleHis 347
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 927
Qy 368 CAGGTGACAGATTCAGAAATCTACCAAGCCCCGGGAGATTCAACAGAGTATAGGTTAGTG 927
Qy 348 LeuLeuLeuGluArgGlyLleGlyLysLysLysSerThrGlnGlyLeuArgAlaIleMet 367
Db |TATTTGCTGCTTTCTTCAAAAGACCCGAAAGAGCCATGAGAGCTTCATCTTGTAAAG 987
Qy 368 AaAaAaArgLysLeuLeuAerGlnCysGlnValProAlaValGlySerLleCysVal 387
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 1047
Qy 388 AlaLeuGlnLeuGlnAerValAlaGlyLysSerValAlaProPheAanGlnThrLeuThr 407
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 1107
Qy 408 GlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCys 427
Db |TCTGTGATCTCTTTCGCTTTTACCTGTTACCTGTTACAGCTGAGGCTGCCAGAGGCTCACT 1167
Qy 428 LeuAanLeuGluGluArgValAlaLeuLysArgPheCysArgMetAlaValGluGlyVal 447
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 1221
Qy 448 TrpAaAaArgLysSerValPheAerPlyAerAerPheMetValGlnGlyLeuGlyGluSer 467
Db |TGGACAGACACATTTGAGATTTTGTGAAGACAGCTCCGAGAAATGGGGTGTGAGAGCT 1281
Qy 468 GlyLeuArgAlaLeuPheHisMetAanLleLeuLeuProAerSerHisCysGluGluTyr 487
Db |GACATCCCTGCGCTGCTGGGACCAAGATATCTTGAAGTACGGGAGCGGTGAAGCTCC 1341
Qy 488 TyrThrPhePheHisLysSerLeuGlnAerPheCysAlaAlaLeuTyrTyrValLeuGlu 507
Db |TACGTGTTCCCTCCACGATGATCCAGAGATCTGTGCGCGCTGTGTTCTATTTGCTCAAG 1401
Qy 508 GlyLeuGlnLleGluPro-----AlaLeuCysProLeuTyr 519
Db |AGCCATCTGATCATCTCTCAACCGAGCTGAGATGTGTACAGAAATGCTAGTTCGAAT 1461
Qy 520 ValGlySerThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisLleHisSerLys 539
Db |TTTGAAGAAAGCAAGAGAGCA-----CATTGAGATT 1491
Qy 540 TrpMetLysArgPheLeuPheGlyLeuValSerGluAerPheValArgArgProLeuGluVal 559
Db |TTTGTGGGGTGTTTTCTAAGCTGGCTTTTAAATGAAAGAAACAAAGAAACTGAGATGCG 1551
Qy 560 LeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisLleTrpValSerLeu 579
Db |TTTGTGGCTTCCAAACGTGCCCAAGAGATAAGCAAGAAATTCACAGTGTCTGAAGAGC 1611
Qy 580 LeuGlyGlnGlnProAanAlaThrThrProGlyAerThrLeuAerAlaPheHisCysLeu 599
Db |TTTGGGAGAGCGTCAATCTCCAGAGACAGGTGATCTTGGGAGATTTTATGCTGCTC 1671
Qy 600 PheGluThrGlnAerPlyGluPheValArgLeuAlaLeuAanSerPheGlnGluValAerTrp 619
Db |TTTGAATGACAGATTCCTGCTTGTGAAGAGCAAGTGAACCTCCCAAGAGAGCTAAC 1731
Qy 620 LeuProLleAanGlnAanLeuAerPheLleAlaSerSerPheCysLeuGlnHisCysPro 639
Db |TTTCATATTATTGACACAGGAGCTTGAGTGTGCTTGCCTTACGCTTAAATATCTGTCTCC 1791
Qy 640 TyrLeuArgLysLleArgValAerValLysGlyLlePheProArgAerGluSerAlaGlu 659
Db |AGCTTGAGAGAACTGTGTTTCCGTTCAAAATCTCTTAAAGAAAGAGTGAACAGAC 1851
Qy 660 AlaCysProValValProLeuTrpMetArgAerPheThrLeuLleGluGlnGlnTrpGlu 679

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Db      1852 TCT-----ACGCGGATTAACGCTCATC-----TGTTGGCAT 1884
Qy      AspPheCySerMetLeuGlyThrHisProHisLeuArgGlnLeuSerLeuGlySerSer 699
Db      1885 CACATCTGCTCTGAGTCCACACCGGAGCCCTGAGAGAGCTCCAGGTCCAGAGACAGC 1944
Qy      IleLeuThrGlnValGlnMetLeuThrLeuGlyValLeuArgHisProThrCysLeu 719
Db      1945 ACCCTCAGCGAGTGCAGCTTTGTGTGACCTGTGTGAATCAGCTGAGGATCCAGCTGTGC 2004
Qy      IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlnValGlnHisLeuThrArg 739
Db      2005 CTTCAGAGAGCTTGGAATAATTAACCTTTCTTTCTGCGCCAGAGCTTCTGCTTTAG 2064
Qy      IleValMetAlaAsnArgAsnLeuArgSerLeuLeuGlnGlyThrHisLeuLeuGln 759
Db      2065 GTGCTCTTTTATCAGCCAGCTTGGAATACTGAGCTTCAACCTCAGAACTCTCTCT 2124
Qy      GlnArgValArgMetAlaCysGlnValLeuLeuHisProLeuCysLeuLeuGlnSerLeu 779
Db      2125 GATGACATCAGAGTCCCTCTGTGATGCTTTGAATACCA----- 2163
Qy      ArgLeuSerCysGlyLeuThrHisAlaCysThrLeuLeuLeuSerGlnIleLeuThr 799
Db      2163 ----- 2163
Qy      ThrSerProSerLeuLeuSerLeuLeuAlaGlnValLeuValThrAspGlnGlyVal 819
Db      2164 -----GCAGGCAAC----- 2172
Qy      MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnValLeuGln 839
Db      2173 -----GTCAAGAGCTAGCGCTGTGTA 2193
Qy      AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db      2194 AATTGTCACTCTCAACCCATGATGTGTGAAGCTTGTGCGCTTCAACCAACAGCAG 2253
Qy      SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlnValAsnGlnGlyValAsnLeu 879
Db      2254 AAGCTGACGTAATCTGAATGTATCTGCAACCAAGTAA---GACACAGCGCGTCCCTTTTG 2310
Qy      CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db      2311 TGTGAAGCTGTGACGCCAGACACGCTCTGTATACCTGATGTGCTTTCTGCGCAC 2370
Qy      LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerThrLeuThr 919
Db      2371 CTCAGCGAGCAGTCTCGGAATACATCTCTGAAATGCTTCTGCGTCAACAGCGCTGCC 2430
Qy      HisLeuSerLeuSerMetAsnProValGlnArgAsnGlnValLeuLeuLeuCysGlnVal 939
Db      2431 TATCTAGACCTCAGTGCATATGCTCTGAAGAGCAAGAGACTGAAACTCTGCGAGAGCC 2490
Qy      MetArgGlnProSerCysHisLeuGlnArgLeuGlnValLeuValCysHisLeuThrAla 959
Db      2491 TTGAAACATCCGAGCTGTGCTGTGATTCATCTGTGTGTAATAATGTTTATACCTGCT 2550
Qy      AlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuLeuSerLeuSer 979
Db      2551 GCTGCTGTGAAGACTGCTGCTCTGCTCATCAGCAATCAAAACCTGAAAGTTTCTGCA 2610
Qy      LeuThrAspAsnAlaLeuGlnValArgLeuGlnValAlaAlaLeuCysGlnGlyLeuValGln 999
Db      2611 ATTGGGTCAATGAATGAATGAGATGCGGTGTGAGCTGTGTGTGCGGCTCTGAGCAT 2670
Qy      LysAsnSerValLeuThrArgLeuGlnValLeuValAlaCysGlyLeuThrSerArgCys 1019
Db      2671 ACGGATTCGCGCTGTGAGAAATTTGTGGTTGGAAGAAATGGGTGAACGAGCACCTGCTGT 2730
Qy      GlnAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039

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Db      2731 AAGGATTCGCGCTGTGCTTCTCAGCTGAGTAAGACCTTGACAGCTCAACCTTG 2790
Qy      AsnAsnPheSerProLeuGlyMetMetLeuLeuCysSerAlaPheAlaCysProThrSer 1059
Db      2791 AACACCTTGACCAACAGAGGAGTGTGTATCTGTGAGGCTTGAGACACCCAGAGTGT 2850
Qy      AsnLeuGlnIleIleGlyLeuThrPheGlnIleProValGlnIleArgLeuLeu 1079
Db      2851 GCCCTGAGGTGCTCGGCTGAGAAACTGATTTTATGAGAAACCCAGACCTTCTG 2910
Qy      GlnGlnValGlnLeuLeuLeuProArgValIle 1091
Db      2911 ACGGCTGAGAAAGAGAAATCTTAACCTGACCATC 2946

RESULT 2
US-10-781-294-23
; Sequence 23, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAD Domain-Containing Polypeptides.
; TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10/781, 294
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965, 621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671, 760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3105)
US-10-781-294-23

Alignment Scores:
Pred. No.: 1,53e-122 Length: 3108
Score: 1320.50 Matches: 348
Percent Similarity: 47.33% Conservative: 175
Best Local Similarity: 31.49% Mismatch: 455
Query Match: 18.67% Indels: 127
DB: 3 Gaps: 19

US-10-066-521-6 (1-1344) x US-10-781-294-23 (1-3108)
Qy      18 LeuTyrgluLeuAspArgGlnGluPheGlnThrPheLeuGlnLeuLeuValSerSer 37
Db      49 TTGAAAGAACTTGAAGAGCTGTGACTGAAGATTCAGG---TTATACCTGGGAGCCGG 105
Qy      38 SerGlnSerThrThrCysSerIleProGlnPheGlnIleGlnValAsnValGlnCys 57
Db      106 ACAAGAGCTGGAGAAAGCAAGATCCCTGGGAGAGCAAGAGAGCGGCTCCCTGGAA 165
Qy      58 LeuAlaLeuLeuLeuHisGlnTyrglyAlaSerLeuAlaThrAlaThrSerIleSer 77
Db      166 ATGGCCAGCTGCTCATACCCACTTCCGGGCCAGAGAGGCTGAGGTTGGCTCTGAGC 225
Qy      78 IlePheGlnAsnMetAsnLeuArgThrLeuSerGlnVala----- 91
Db      226 ACCTTTGAGCGGATTAACAGAAAGGACCTGTGGAGAGAGAGACAGAGAGAGACCTGGTG 285
Qy      92 -----ArgAspAsnMetLeuValIleSerGlnAlaMetGln 104

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Db      286 AGGATGCCAGAAACCTACAGGACTATGTCGACAGAAATTCCGCTCATGGAAGAC 345
Qy      105 GluGluValThrAlaAlaGlu-----ThrGluGluGluGluIleSerGlnAlaMet 121
Db      346 CGCAATGCGCGCTAGGGGAATGTGTCAACTCAGCCACCGGCTCTGCTGCTG 405
Qy      122 GluGluGluGluValThrAlaAlaGluThrGluGluGlu-----Gly 135
Db      406 GTGAAGGACACTCAAAACCCATGACAGTCCAGAGCTTCTTGACACAGCCGGGA 465
Qy      136 HisGlyGlyAspThrTrpAspTyrTyrSerHisValMetThrTyrPheAlaGluGlu 155
Db      466 CAGCGGAGGACCGTGGGACACAGGCTAGCCCATCAAGATPAGAGACCTCTTGAGCCA 525
Qy      156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
Db      526 GACGAGGAGCGC-----CCCGAG----- 543
Qy      176 GluValaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyTyr 195
Db      544 -----CCACCGCGCACCGTGTGTCATGACAGGCGCG 573
Qy      196 SerGlyTyrIleGlyTyrSerAlaAlaLeuAlaArgArgIleValIleuCyTrpAlaGluGly 215
Db      574 GCAAGGATAGGCAAGTCCATGCTGCGACACAGAGTGATGCTGAGCTGGCGGACGGGAG 633
Qy      216 LeuTyrGluGlnMetPheSerTyrValPhePheLeuProValArgIleMet---GlnArg 234
Db      634 CTCTTCAGAGCGAGATTTGATCTCTTCACTCACTGACAGGAGATGAACCAAGT 693
Qy      235 LysLysGluSerSerValThrGluPheIleSerArgIleTrpProAspSerGlnAlaPro 254
Db      694 GCCACGGAATGACATGACGACAGCTCATCTTCACTGCTGCTGCTGAGCCAGGCGCCT 753
Qy      255 ValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspArg 274
Db      754 CTCAGAGAGTCAATCCGAGTTCCGAGCGCTCTTTCATCATGACGCGCTTGATGAG 813
Qy      275 Leu---GlySerValIleuAsnAspThrTyrIleuLeuCyLysAspTrpAlaGluTyrGln 293
Db      814 CTCAGGCTTCTTCCAGATCTCTCAGAGAACCTGTGCTGCTGCTGAGAGAAACCG 873
Qy      294 ProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeu 313
Db      874 CCCACGAGAGCTCTTTCACGCTTAATGTGAAGAAAGCTGCTCCCTGAGCTATCTTTG 933
Qy      314 IleValThrValAlaArgAspValGlyThrGluLysLeuIleuSerGlnValIleSerProArg 333
Db      934 CTCATCACACACACGCGCCACGCGCTTGTGAAGAGCTCCACGCTGCGAGCACCCGAG 993
Qy      334 TyrIleuLeuValArgGlyIleSerGlyGluGlnArgIleHisIleuLeuGluArgGly 353
Db      994 CATGTGAGATCTGCGCTTCTGTGAGGCGAAGAAAGAAAGAAATCTTCAACAGATATTTC 1053
Qy      354 IleGlyLysIleGlnIleuSerThrGlnGlyLeuArgAlaIleMetAsnAspArgLysLeu 373
Db      1054 CACAAATGACAGACGCGCGGCGCAAGTCTTCAATTACGTGAGGACACACAGCCCTCTTC 1113
Qy      374 AspGlnCySerGlnValProAlaValGlySerLeuIleCyValAlaLeuGlnLeuGlnAsp 393
Db      1114 ACATATGCTTCCGCTCCCTGTGTGTGCTGTGTGTGTACTCTGCTCCAGCACACACTG 1173
Qy      394 ValValIleGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPhe 413
Db      1174 GAGGCTGTGGGCGCTGTGTGAGACAGACGTCCAGACCAACCACTGTGACATGCTCTG 1233
Qy      414 ValPheHisGlnLeuThrProArgGlyValValaArgArgCysLeuAsnLeuGluArg 433
Db      1234 CTGCTGAGTCTGATGCAACCCAGACCGCGGCGCGCC-----CTCCAGCCCCCA 1284
Qy      434 ValValLeuIleuArgMetCysArgMetAlaValGluGlyValTrpAsnArgLysSerVal 453

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Db      1285 CCCAACAGAGAGGCTGTGCTCTTGGCGGACAGATGAGGCTGTGAATACGAAATCTTA 1344
Qy      454 PheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPhe 473
Db      1345 TTGAGGAGGACGAGACCTCCGGAACACAGGCTTAGACGGGAGAGACGTTCTGCTCTTC 1404
Qy      474 HisMetAsnIleLeuLeuProAspSerHisCySerGluGluTyrTyrThrPhePheHisLeu 493
Db      1405 AACATGAACATCTTCCAGAAAGACATCAACTGTGAGAGGTATACAGCTTCATCCACTTG 1464
Qy      494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGlu-----GlyLeu 509
Db      1465 AGTTTCAGAGATCTTGTGAGCTATGCTATTAATCTTGACAGGAGGCGGAGCGGCGCA 1524
Qy      510 GluIleGluProAlaLeuCyProLeuTyrValGluTyr-----ThrLysArgSerMet 527
Db      1525 GGGCCAGACAGGACGTGACAGGCTGTGACCGATGACCGCTTCTTGAAAGAGCTTC 1584
Qy      528 GluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGly 547
Db      1585 -----CTGCACTCACAGCGCTTCTGTTTGA 1614
Qy      548 LeuValSerGlyAspValaArgArgProLeuGluValLeuLeuGlyCysProValProLeu 567
Db      1615 CTCTGAAACGAGGACACAGAGCCACCTGGAAGAAGATTCTGTGTAAGAGTCTGCGG 1674
Qy      568 GlyValIleGlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThr 587
Db      1675 CACATCAAGATGAGACTGTGTCAGTGGATTCAAAGCAAGCTCAGACGACCGCTCCACC 1734
Qy      588 ThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPhe 607
Db      1735 CTGAGAGGCGCTCTTGAGATTCTTCACTGCTGTGATGACAGATTCAGAGAGAGAGTTT 1794
Qy      608 ValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeuPro---IleAsnGlnAsnLeu 626
Db      1795 ATCCAGAGGCGCTGAGCCACTTCCAGTGATGTGTGTCGCAACATGTCTCCAGATG 1854
Qy      627 AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
Db      1855 GAGCAGATGTCTCTCTGTTCTGTGAAGCGCTG----- 1890
Qy      647 AspValIleGlyIlePheProArgAspGluSerAlaGlnAlaCysProValValProLeu 666
Db      1891 -----AGGAGCGCCAGCGTGTG----- 1908
Qy      667 TrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGly 686
Db      1908 ----- 1908
Qy      687 ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
Db      1909 -----CACTTG-----TAGGGCGCACCTTACAGCGGCGGAGAGAC 1947
Qy      707 LysThrLeuCyValAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArg 726
Db      1948 CGGCGAGGTGTCTCCGACGAGGCGCAC---ACCTGTGTGTGAGCTCAGACCAAGAGG 2004
Qy      727 AsnAlaGlnIleThrProGlyValaGlnHisLeuTrpArgIleValaMetAlaAspArgAsn 746
Db      2005 ACCGTTGTGTGACCGCTACAGTAAATCTGTGACAGCGCCCTGTGACCAATTCAAAC 2064
Qy      747 LeuArgSerLeuAsnLeuGlyGlyThrHisIleuLysGluGluLysValaArgMetAlaCys 766
Db      2065 CTGATGAGCTGTCTGTGACCAAAATGCGCTGGACGCGGGGGGTGAAGCTGTCTGT 2124
Qy      767 GluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeu 786
Db      2125 CAAGACTCAGACACCCCACTCAACTCAGAACTGAGAGCTGAAAGAGTCCGCGATC 2184
Qy      787 ThrHisAlaCysTyrTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSer 806
Db      2185 TCCAGCTCAGCGCTGCGAGGACCTTGTGAGCTCTCATAGCCAAATGAATTTGACAAAG 2244

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QY 807 LeuSerLeuAlaGlyValMetThrAspGlnGlyValMetProLeuSerAspAlaLeu 826
DB 2245 ATGATCTCAAGTGGCGGCTGGATTCACGAGGATGCTGCTGGAGGGCTG 2304
QY 827 ArgValSerGlnCysAlaLeuGlnLeuLeuLeuGlnAlaProCysGlyIleThrAlaThr 846
DB 2305 CGGATCCCGGATCGAGCTGCAATGATTGAGTGAAGAGTGCACGTGAGTCCGG 2364
QY 847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
DB 2365 GCTTGTCAAGAGATGCTTGTGCTCGGACCAACCACTGCTGAGTGAAGTGA 2424
QY 867 SerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
DB 2425 ACAGAAATGCACTGAGAGATTTGGGCTGAGATTACTATGACAGGAGTGAAGGACCA 2484
QY 887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
DB 2485 GTCTGCAGACTACGAGACTTGTGCTGAAAGATCTGCCCTCAGCTGCTGCCCTGAC 2544
QY 907 PheLeuAlaLeuAlaLeuMetCysLeuSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
DB 2545 GAGCTGGCTCAACTCTCAGTGTGAACCAAGAGCTGAGAGAGCTGAGCTGAGCTGAT 2604
QY 927 ProValGlnAspAsnGlyValIleLeuLeuCysGlnValMetArgGlnProSerCysHis 946
DB 2605 GAGCTGGGAGCTCGGGGTGTGCTGTGTGTGAGGGCTCGAGGATCCACGTCGAC 2664
QY 947 LeuGlnAspLeuGlnLeuValIleCysHisLeuThrAlaAlaCysGlnGlnSerLeuSer 966
DB 2665 CTCGAGACCTGCGGCTTGGGATCTGCGGCTGCGGCTGCGGCTGAGGCTTCTTCT 2724
QY 967 CysValIleSerArgSerArgHisLeuLeuSerLeuAspLeuThrAspAsnAlaLeuGly 986
DB 2725 GTGGGTCTCCAGCCACACCACTCCGGAGCTGAGCTTGAAGTTCAACGACTGGGA 2784
QY 987 AspGlyGlyValAlaAlaLeuCysGlnGlyLeuGlyValIleValIleValIleValIle 1006
DB 2785 GACTGGGGCTGTGTGCTGCTGCTGAGGCTGCAACATCCGCTGCAAGCTTCAGAA 2844
QY 1007 LeuGlyLeuValAlaCysGlyLeuThrSerAspCysCysGlnAlaLeuSerLeuAlaLeu 1026
DB 2845 CTGTGGCTGATGATGCTGTGCTTCAAGCCAGGCTGTGAGAACTTTACTTCAACCTG 2904
QY 1027 SerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnAspSerProIleGly 1046
DB 2905 GGAATCAACAGACCTTGAACGACCTTACCTGACCAACACGCTGAGGGAGACAGGT 2964
QY 1047 MetMetLeuLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu 1066
DB 2965 GTCCAGCTCTTGGAGGGCTGAGCCATCTGTGCTGCAAACTCCGAGTCTTC 3018
QY 1067 TrpIleTrpGlnIleProValGlnIleArgIleLeu-----LeuGlnGlnVal 1082
DB 3019 -----TGGTATTTGGAGTGAAGCTGAATTAATTAATCAACCAAGTAGTGGACGCTT 3072
QY 1083 GlnLeuLeuIlePro 1087
DB 3073 CGAGTAAACAAACCT 3087

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RESULT 3
US-09-996-617-5
; Sequence 5, Application US/0996617
; Patent No. 6953657
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-340001
; CURRENT APPLICATION NUMBER: US/09/996,617
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 09/931,071

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; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/428,252
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-996-617-5

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Alignment Scores:
Pred. No.: 2,78e-85 Length: 4287
Score: 955.00 Matches: 394
Percent Similarity: 36.89% Conserved: 200
Best Local Similarity: 24.47% Mismatches: 473
Query Match: 13.50% Indels: 545
DB: 3 Gaps: 57

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US-10-066-521-6 (1-1344) x US-09-996-617-5 (1-4287)

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DB 13 GCTGGGGGCGGCTGGCTGCTTACTTGAAGTTCCTGAAGAGAGAGAGAGAGAGAGTTC 72
QY 30 LysGlnLeuLeuValIleValIleSer-----SerLeuSerThrTrpCysSerIleProGlnPhe 48
DB 73 CAGCTTCTCTCGCCAAATGAAGGCGCATCCAGAGCTTTCGGGTGAAGACACCGCTCAG 132
QY 49 GlnIleGlnAsnAlaAsnValAlaGluCysLeuAlaLeuLeuHisGlnTrpTrpGlyAla 68
DB 133 CCAAGAAAGAGAGATGAGATGAGTGGCTCTGATCTGTGTGGCTCAG---TATGGGAG 189
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGlnAsnMetAsnLeuArgThrLeuSer 88
DB 190 CAGGGGCTGTGAGACTTACCTGATCTGAGAGAGATGGGGCTGAGGTCACTGTGC 249
QY 89 GlnIleValAlaArgAspAsp----- 94
DB 250 GCCCAAGCCAGAGAGAGGGGAGGCCACTCTCCATTCCCTACAGCCCAAGTGAACCC 309
QY 94 ----- 94
DB 310 CACTGGGGTCTCCAGCCAAACCACTTCAACCGGATGCTAATGCTTGAATTCATGA 369
QY 94 ----- 94
DB 370 TTGGCGGGGGGTGACCCAGGGCTCAGAGAGAGAGGTTTGAAGACAGCTGCTGACACA 429
QY 95 -----MetIleValIleSerGlnAlaMet----- 102
DB 430 TCTGAGCCCGCTGAGAGAAATCTCTGCTCACTCTTCAAGACTTTCGAAGCTCC 489
QY 102 ----- 102
DB 490 CCAAGCATGAGTCTCAAGCCAGAGATCAACCAAGCCGCCCAATCCACAGACATGCTG 549
QY 103 -----GlnGlnGlnGlyAla----- 107
DB 550 GGGAGCTGGGATCCCACTCAAGCCAGGCTGAGCAACCAAGAGAGAGAGGCTCTGGG 609
QY 108 -----ThrAlaAlaGlnThrGlnGln 114
DB 610 ACCCAATGCTCTGATGAATAAGTCAAGAAATTTACTACAGAAATCAAGAGAAAGAGG 669
QY 115 GlnGlnIleSerGlnAlaMetGlnGlnGlnGlnAlaIleAlaGlnIleThrGlnGln 134
DB 670 AAGAGAAATCAAGAGAAAGAGAGGCCCCCATGGGAGGGGTGTGAGAAAGCCCCCAGAG 729
QY 135 GlnIleGlnGly----- 138

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Db 730 GCGCACACAGCCTACAGCCCAACCAACCATGAGAGCCTTCTGTAGAGAGAGCCTC 789
 Qy 139 ---AspThrTrpAspTrpIleuSerHisValMetThr---LysPhe----- 151
 Db 790 TGTTCACATAGCCCTGGAAAAATGAGGATTTTAAACCAAAAATTTCACACAGCTGTACTT 849
 Qy 152 -----AlaGluGluIleuAspValArgArgSerPheGluAsnThr 164
 Db 850 CTCAAAGACCTCACCCCAAGACCAAGATCCCTGGTCAAGAGAGAC----- 897
 Qy 165 AlaAlaAspTrpPro----- 948
 Db 898 -----TGGCTGTATGTGTAGAGAGAAATGACAGACATTTAATTGATGATGAGAC 948
 Qy 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValIleu 192
 Db 949 TTATTGGCCAGGCTGGATATCCCA-----GAACTCGCATATGATATCTG 996
 Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCystrpAla 212
 Db 997 CAGGGGCTGTGGAAATTGGGAATCAACTGGCCAGGACGTGAGAGAAAGCCTGGGGG 1056
 Qy 213 GlnGlyLysLeuTrpGlnGlyMetPheSerTrpValPhePheLeuProValArgGluMet 232
 Db 1057 AGAGCCAGCTGTATGGGAGACCGCTTCACGATGCTTCTTCACTGACCTGCAGAGAGCTG 1116
 Qy 233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProArgSerGln 252
 Db 1117 GCCAGTTCACAGGCTGAGTCTGCTGAGCTCATCGAAAAGATGGACAGCCATCCG 1176
 Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleLeuAspGlyPhe 272
 Db 1177 GCTCCCATAGACATCTGTCTTACAGCCAGAGCGGCTGCTTCATCTCGATGGGTGTA 1236
 Qy 273 AspAspLeuGlySerValIleuAsnAsn---AspThrLysLeuCystrpAspTrpAlaGlu 291
 Db 1237 GATGAGCCAGGATGAGTCTTGCAGAGCCAGATCTGTCTGCTGCTGCTGCTGCTGAG 1296
 Qy 292 LysGlnProProPheThrIleuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
 Db 1297 CCACAGCCGGGAGATGACATCTGCGGCACTTGTCTGGGAAAAATTAATCTCCGAGGCA 1356
 Qy 312 PheLeuIleValIleThrValArgAspValGlyThrGluLysLeuLysSerGluValSer 331
 Db 1357 TCCCTCTGATCAAGGCTCGGACCAAGCTGTGCAAAACCTCATCTCTTTGGAGACAG 1416
 Qy 332 ProArgTrpLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGlu 351
 Db 1417 GCAGGTGGGTAGAGTCTGGGGTCTCTGAGTCCAGAGAAAGAAATTTCTACAGA 1476
 Qy 352 ArgGlyIleGlyGluHisGlnLysThrGlnLysLeuArgAlaIleMetAsnAsnArgGlu 371
 Db 1477 TATTTCACATGTAAGGCAAGCAATTAGACCTTTAGGTTGGTTCAAATCAAAAGAG 1536
 Qy 372 LeuLeuAspGlnCystrpValProAlaValGlySerLeuIleCystrpAlaLeuGlu 391
 Db 1537 CTCGGGCGCTGTGTCTTGTGCTGGGTGTCTGCTGCTGCTGCTGCTGCTGATGACAG 1596
 Qy 392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrIleu-----Leu 409
 Db 1597 CAGATGAGCGGAGAAAGAACTCACATGACTTCAGAACCAACCAACCCCTGTCTTA 1656
 Qy 410 HisAlaIlePheValPheHisGlnLeuThrProArgGlyValValArgArgCystrpLeu 429
 Db 1657 CATTAACCTGGCCAGGCTCTCAAGCTCAGCCATTGGGA----- 1695
 Qy 430 LeuGluGluArgValValLeuLysArgPheCystrpMetAlaValGluGlyValTrpAsn 449
 Db 1696 -----CCCAAGCTCAGAGACCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
 Qy 450 ArgLysSerValPheAspArgLysAspAspLeuMetValGlnGlyLeuGluGlyLysSerGlu 469
 Db 1744 AAAAAGACCTTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1803

Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCystrpGlu 485
 Db 1804 TCACACCTTTGTAAGATGGGATATTCTTCAAGAGACCCCATCCCTGTGACG----- 1854
 Qy 486 GluTrpTrpThrPhePheHisIleuSerLeuGlnAspPheCystrpAlaIleLeuTrpVal 505
 Db 1855 -----TACAGCTTCATTCACCTGTGTTCCAAAGATCTTGTTCAGAGATGCTTATGCT 1908
 Qy 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCystrpProLeuTrpValGluLysThr 523
 Db 1909 TTGAGGATAGAGAGGAGAGGATTAACATTTATTTGATCATCATATTTGGAAAAAGC 1968
 Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
 Db 1969 CTAGAGCA-----TATGAAATATACATGAGCTGTGTTGGGCGATCA 2007
 Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
 Db 2008 ACCACAGTTCCTTATTTGGGCTGTATGATGATGAGGGAGAGAGATGAGAGACATC 2067
 Qy 561 LeuGlyCystrpProValProLeuGlyValLysGlnLysLeuLeuHisIleTrpValSerLeu 580
 Db 2068 TTTCACCTGCGGCTGTCTGAGGG-----AGAACTGATGCAAGTGGTCCGCTCCG 2121
 Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCystrp 598
 Db 2122 CAGCTGCTGTGAGCCACAC-----TCTGTGAGTCCCTTCACATGCTC 2163
 Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
 Db 2164 TTGTACAGACTGGGAAACCAACGTTCTGTACACAACTGATGAGCCCATTTGAAAGAAATG 2223
 Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCystrpGlnHisCystrp 638
 Db 2224 GGCATGTGTGTGAAGAAACAAKACATGAGAGCTTTGTGTGCTGCTTGTGCATTAATTCAGC 2283
 Qy 639 ProTrpLeuArgLysValLeuArgValAspValLysGlyIlePheProArgAspGluSerAla 658
 Db 2284 CGCACGTGAAGAAAGCTTCAGCTG---ATTGAGGGC-----AGGACAGCAGATCA 2331
 Qy 659 GluAlaCystrpProValValProLeuTrpMetArgAspLysThrLeuIleGluGlnTrp 678
 Db 2332 ACATGAGCCCAACCAAGTATGATGCTGTTCAGAGTGGTCCCAAGTCAAGATGCCATTGG 2391
 Qy 679 GluAspPheCystrpMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySer 698
 Db 2391 ----- 2391
 Qy 699 SerIleLeuThrGluArgAlaMetLysThrLeuCystrpAlaLysLeuArgHisProThrCystrp 718
 Db 2391 ----- 2391
 Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnIleLeuTrp 738
 Db 2392 -----CAGATTCTCTGCT 2403
 Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisIleLeuLys 758
 Db 2404 TCCGTCTCAAGGTCAACCAAAACCTGAGAGAGCTGAGACTTAAGTGAAGAACTGGTGAAGC 2463
 Qy 759 GlnGluAspValArgMetAlaCystrpAlaLeuLysHisProLysCystrpLeuLeuGluSer 778
 Db 2464 CACTGTCAAGTGAAGAGTCTTTGTAGACCTGTGAGAGCGCTGCTGCTGCTGCTGAGAACCC 2523
 Qy 779 LeuArgLeuAspCystrpGlyLeuThrHisAlaCystrpTrpLeuLysIleSerGlnIleLeu 798
 Db 2524 CTGGG----- 2529
 Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818
 Db 2530 -----TTGGCTGGC----- 2538

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Qy 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysValaLeuGlnIleuLeu 838
Db 2538 -----
Qy 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db 2539 -----TGTGGCTTCAGAGCTGAGAGCTGCAAGAGCCTTGGCTTGGAGTCAAGAGCCAAAC 2592
Qy 859 ArgSerLeuThrAlaLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValaAsnLeu 878
Db 2593 CAGAGC-----
Qy 879 LeuCyAspArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
Db 2598 -----
Qy 899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918
Db 2599 -----CTG 2601
Qy 919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValaLeuLeuLeuCysGlu 938
Db 2602 ACCAGAGCTGAGACTGACCTTAATGTCTCAAGATGCTGAGAGCCAAACACCTTGGCCAG 2661
Qy 939 ValMetArgGluProSerCysHisLeuGlnAspLeuGlnLeuValaLeuCysHisLeuThr 958
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Qy 959 AlaAlaCysCysGlnSerLeuSerCysValaIleSerArgSerArgHisLeuIleSerLeu 978
Db 2722 TCTAGCTCTGCCAGAGCTGAGCTGCTGTGCTTATGCGACAGCCAGCTGAGAGAGCTA 2781
Qy 979 AspLeuThrAspAsnAlaLeuGlyAspGlyValaAlaAlaLeuCysGlnGlyLeuIle 998
Db 2782 GACCTGACAGAGAAACAACTGGATGACCTGGCGCTGACCTGCTGTGAGAGGCTTCAAG 2841
Qy 999 GlnIleAsnSerValLeuThrArgLeuGlnIleuValaCysGlyLeuThrSerAspCys 1018
Db 2842 CATCTGCTGCMAACTATACGCTGAGGCTGAGACCAAGCAACTGTGATGATGATG 2901
Qy 1019 CysGlnAlaLeuSerLeu-----AlaLeuSerCysAsnArgHis 1031
Db 2902 AGCGAGAACTGAGAGCCCTGAGAGAGAAACCTCAAGCTGTATCTTCAAGAGAGG 2961
Qy 1032 LeuThrSerLeu-----AsnLeuValGlnAsnAspHe 1042
Db 2962 AAACCAAGTGTGATGACCCCTACTGAGGAGCTGATACCGAGAGATGATGATGACCA 3021
Qy 1043 SerProIleGlyMetIleLeuCysSerAlaPheAlaCys-----ProThrSer 1059
Db 3022 TCTTCACTCAAGCGGAGAGCTGAGATCAGAGAGGCGGCTTCCCATGTTGCTCAAGCT 3081
Qy 1060 AsnLeuGlnIleIleGlyLeuThrIleuTrpGlnIleProValGlnIleArgIleuLeu 1079
Db 3082 AATCTCAAACTCTGAGAGTGAAGAG--ATCTTCCCA-----ATTGCTGAGATGCA 3132
Qy 1080 GlnGlu-----ValGlnLeuLeu-----LysProArgValaIle 1091
Db 3133 GAGGAAAGCTCCCAAGAGGTAGTACCGGTGAACTTGTGTGCTGCTTCTCTGCTCT 3192
Qy 1092 AspGlySerTrpHisSerPheAspAlaAspAspArgHisIleGlyLeuThrPheArg 1111
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Qy 1111 GluLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGluGlnIle 1131
Db 3235 TTCTGGGGCCCAACGGGGC-----CTGTGGCTACTGAGTAGTACAA 3279
Qy 1131 slyValArgValSerLeuLeuAlaGlyAspPheIleSerSerThrArgPheAlaLysSerIle 1151
Db 3280 GAAAAAGA-----ACTGTGACCGAGTTTCACT---TCCCT 3309
Qy 1151 uCybLeuAlaThrAlaAsnGlyIleSerGlnArgValaAspAsnVal-GluGlnSerSerP 1171

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Db 3310 GTAGCTGGCTCTCAAGCTGGCCCAACA---CGGGTCTGTGCTTGTGATGAGAGAGCG 3366
Qy 1171 roGlnProMetAlaGlyThrGlnHisIleGlnAspIleuMetLeuSerValaGly---TyrS 1190
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Qy 1190 ergIValaTrpSerGlyThrAlaGluLeuGlnGlyLeuGlySerAsnSerAlaAspHis 1210
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Qy 1210 sPnIleGlyMetAlaTrpSerLeuGlyArgGluLeuSerSerArgGlyLeuCys--- 1228
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Qy 1229 --ProthValLeuMetThrThrAlaValCysProGlnHisTrpGluArgLeuIleSer 1248
Db 3514 CTCCAAAGGGG--GCCATGTGACACATCTCTGT---TCCAAATGGCCCACTTAAAGAGA 3569
Qy 1248 TGGly----- 1249
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Qy 1249 ----- 1249
Db 3630 CAGCTTCCCTTGGGAGTCTCTGAAATGATCATATGCTCCCTGCTCATTTCC 3689
Qy 1250 -----TrpCys-----LeuAsnSerAlaAspAspHis 1259
Db 3690 CGTCACTGTGTGTGTGTTTATTCACACCGGCTCATCTAGAGATCATCTTCCACT 3749
Qy 1259 er-----GlyValSerTrpSerLeuGlyAlaAlaGlyL 1270
Db 3750 TCACTTATCCCAAGTACTGCTCATCTGAGAGAGATGAGC-----TGTGCTA 3800
Qy 1270 euGlnGlyLeuValSerAsnSerAlaAspAspHisSerGlyValaAla---TrpSerLeu 1289
Db 3801 TCGAAGCCCTGAGAGAACAGCAGTGTCTCGAGTTTACGTGTGAGCCACTTGGAGTACAG 3860
Qy 1289 IyAlaAla-----GlyLeuGlnGlyLeu----- 1296
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Qy 1307 ValSerTrpSerLeuGlyAlaAlaGlyLeuGlnGlyLeuValSerAsnSerAlaAsp 1326
Db 3981 ACCTTGAATGCCCCGAGTGTCTGCACTTGTGTGACCAAGTATCGAGAGAGCTGATAGC 4040
Qy 1327 HisSerGlyValSerTrpSerLeu 1334
Db 4041 CCGAGTGAATCGG--TGGAGGTTG 4063

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RESULT 4
 US-09-388-221B-1
 / Sequence 1, Application US/09388221B
 / Patent No. 6818750
 / GENERAL INFORMATION:
 / APPLICANT: Reed, John C.
 / TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
 / FILE REFERENCE: P-1/L 3650
 / CURRENT APPLICATION NUMBER: US/09/388,221B
 / NUMBER OF SEQ ID NOS: 30
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 1
 / LENGTH: 4422
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS


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Qy      524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
Db      1969 CTAGAACCA-----TATGAAATACATGGCCCTGTGTTGGGGCATCA 2007
Qy      541 MetLysArgPheLeuPheGlyLeuValSerGluLysValArgArgProLeuGluValLeu 560
Db      2008 ACCACAGCTTTCCCTTATGGGCTGTAAAGTATGAGGGGAGAGAGATGAGAAACATC 2067
Qy      561 LeuGlyCysProValProLeuGlyValIysGlnLysLeuHisIleTrpValSerLeuLeu 580
Db      2068 TTTCACGTCCGGCTGTCTCAGGGG-----AGAAACCTGATGACATGGGCTCCGCTCC 2121
Qy      581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLysAspAlaPheHisCys 598
Db      2122 CAGCTGCTGTGACCCACAC-----TCTGTGAGCTCCCTCCACTGC 2163
Qy      599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db      2164 TTGTACAGACTCCGAAACAAACCTTCTGTGACACAGATGAGCCCATTTGGAAATG 2223
Qy      619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
Db      2224 GGCAATGTGTAGAAACAGACATGAGACTTTAGTGTGCACATTTCTGCATTAATTCAGC 2283
Qy      639 ProGlyLeuArgLysIleArgValAspValIysGlyIlePheProArgAspGluSerIle 658
Db      2284 CGCCACGTGAAGAGCTTCAGCTG-----ATTGAGGGC-----AGGCACACAGATCA 2331
Qy      659 GluLacCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678
Db      2332 ACAAGAGCCCCACAGCTGATGCTGTTCACAGTGGGCTCCAGTACAGATGCCATTGG 2391
Qy      679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLysSer 698
Db      2391 ----- 2391
Qy      699 SerIleLeuThrGluArgAlaMetLysThrLeuCysValIleLysLeuArgHisProThrCys 718
Db      2391 ----- 2391
Qy      719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738
Db      2392 -----CAGATTCTCTTC 2403
Qy      739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeuLys 758
Db      2404 TCCGTCCTCAGAGTACACAGAAACCTGAAGAGCTGAGACTTAAGTGAAGAACTCGCTGAGC 2463
Qy      759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisIleProLysCysLeuLeuGluSer 778
Db      2464 CACTCTGCAAGTGAAGTCTTTGTAAACCCCTGAAGACCCCTCGCTGCTCTCTGAGAGCC 2523
Qy      779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysIleCysIleLysSerGlnIleLeu 798
Db      2524 CTGGCG----- 2529
Qy      799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818
Db      2530 -----TTGGCTGGC----- 2538
Qy      819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838
Db      2538 ----- 2538
Qy      839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db      2539 -----TGTGGCTCAAGCTAGAGACTGCAAGACCTTGGCTTGGGCTGAGAGCCAAC 2592
Qy      859 ArgSerLeuThrHisIleLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeu 878
Db      -----

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Db      2593 CAGACC----- 2598
Qy      879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
Db      2598 ----- 2598
Qy      899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918
Db      2599 -----CTG 2601
Qy      919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGly 938
Db      2602 ACCAGAGCTGAGCTGAGCTTCAATGTGTCTACGGATCTGTGAGCCAAACACTTTGCCAG 2661
Qy      939 ValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThr 958
Db      2662 AGACTGAGACAGCCGAGCTGACACTACAGAGTGCAGAGCTGCAGCTGAGCTGAGCTGAG 2721
Qy      959 AlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978
Db      2722 TCTGACTGCTGCCAGACCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2781
Qy      979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGluGluGlyLeuLys 998
Db      2782 GACCTGACAGACAAACACCTGATGACGTGGCGCTGAGCACTGCTGTGTGTGTGTGTGTGT 2841
Qy      999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysValCysGlyLeuThrSerAspCys 1018
Db      2842 CATCTGCTGCTCAAACTCATACGCTGTGGGCTGTGACCCAGACACTGTAGAGATGAGATG 2901
Qy      1019 CysGluAlaLeuSerLeu-----AlaLeuSerCysAsnArgHis 1031
Db      2902 AGCAGAGAACTGAGAGCCCTGAGACAGAGAAACCTGACTGTCTATCTTGCAGAGAGG 2961
Qy      1032 LeuThrSerLeu-----AsnLeuValGlnAsnAspPhe 1042
Db      2962 AAACCAAGTGAATGACCCCTTACGTAGGGCTGTGATACGGAGAGATGATGAATATGACA 3021
Qy      1043 SerProLysGlyMetMetLysLeuCysSerAlaPheAlaCys-----ProThrSer 1059
Db      3022 TCTTCATCTCAAGCCGACAGACTGTGATCAGAGGGCGGCTGCCATGTTCCTCAGGCT 3081
Qy      1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTrpProValGlnIleArgLysLeuLeu 1079
Db      3082 AATCTCAAACTCTGACAGCTGAGCAAG-----ATCTTCCA-----ATTGCTGAGATTGCA 3132
Qy      1080 GluGlu-----ValGlnLeuLeu-----LysProArgValIle 1091
Db      3133 GAGGAAAGCTCCCAAGAGTATACCGGTGAACTCTGTGCGCTCTTCCTGCTGCTCT 3192
Qy      1092 AspGlySerTrpHisSerPheAspGluAspArgHisIleLysIle-GlyLeuThrPheArg 1111
Db      3193 CAAAGGAGACTGTGATAC-----AAGCTTTGGGACTGACGATGAC 3234
Qy      1111 GlnLeuProLysSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGluGlnLys 1131
Db      3235 TTTCGGGGCCCCAGGGGC-----CTGTGGCTACTAGAGTATTGACAAA 3279
Qy      1131 GlyArgValSerLeuLeuAlaGlyAspPheLysSerThrArgPheAlaLysSerIle 1151
Db      3280 GAAAAA-----ACTGTATCCAGATTCACT--TCCCT 3309
Qy      1151 CysLeuAlaThrAlaAsnGlyGluSerGlnArgValAspAsnVal-GluGlnSerSerP 1171
Db      3310 GTAAGTGGCTCTTACCGCTGGCCCAACA-----CGGGTCTCTGCTTTGTGTGAGAACAG 3366
Qy      1171 ArgIleProMetAlaGlyThrGlnHisLysLysAspLysMetLeuSerValGly--Tys 1190
Db      3367 GTGAC-----CGTTGAGATTGAATCTGTGTGTGTGAGAACAGATTTC 3405
Qy      1190 ArgIleAlaTrpSerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaAspHisAla 1210
Db      3406 CTGGGTGAGATCAACCCACAGACACAGCTGAGTGT--GGCAGGGCTCTGTGAGATTC 3462

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QY 1210 sphisgylgylmetatpserleuglyargylleuSerSerArglyLeuCyse----- 1228
DB 3463 AA-----GGCTAGAGCTGAGCTGGA---AGCTGTGACCTCCCTCACTTTGGCT 3513
QY 1229 --ProThrValLeuMetThrThrAlaValCysProGlyHisTrpGluArgLeuGlySerA 1248
DB 3514 CTCGAGGGG--GCCATGTGACACATCCCTGT---TCCAATGCGCCCACTTTAAAGAGA 3569
QY 1248 rglly-----TTPCySLeuAnSerAlaAspAspHisSerGlyValSerTrpSer 1264
DB 3570 GGGAGTGTCTCTGG-----AGAGCCAGCCAGGGGTGAGC 3604

RESULT 5

US-09-996-617-1
/ Sequence 1, Application US/09996617
/ Patent No. 6953657
/ GENERAL INFORMATION:
/ APPLICANT: Bertin, John
/ TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
/ TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
/ FILE REFERENCE: 07334-340001
/ CURRENT APPLICATION NUMBER: US/09/996,617
/ CURRENT FILING DATE: 2001-11-27
/ PRIOR APPLICATION NUMBER: 09/931,071
/ PRIOR FILING DATE: 2001-08-15
/ PRIOR APPLICATION NUMBER: 09/428,252
/ PRIOR FILING DATE: 1999-10-27
/ PRIOR APPLICATION NUMBER: 09/340,620
/ PRIOR FILING DATE: 1999-06-28
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 5444
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: CDS
/ LOCATION: (523) ... (4809)
US-09-996-617-1

Alignment Scores:

Pred. No.: 4,28e-85 Length: 5444
Score: 955.00 Matches: 394
Percent Similarity: 36.89% Conservative: 200
Best Local Similarity: 24.47% Mismatches: 473
Query Match: 13.50% Indels: 545
DB: 3 Gaps: 57

US-10-066-521-6 (1-1344) x US-09-996-617-1 (1-5444)

QY 11 SerTrgLyLeuGlnTrpCySLeuTrgLyLeuAspLyGlnGluPheGlnThrPhe 29
DB 535 GCGTGGGGCGCGCTGCTTACTTGAAGTCTCTGAAGAGGAGGAGCTGAAGAGCTTC 594
QY 30 LysGlnLeuLeuLeuLysLysSer---SerGlnSerThrThrCysSerIleProGlnPhe 48
DB 595 CAGCTTCTGCTCGCATTAAGCCGACCTCCAGAGCTCTTGGGTGAGACACCGGCTCAG 654
QY 49 GlnIleGlnAsnAlaAsnValGluCySLeuAlaLeuLeuLeuHisGluTrpTrgLyAla 68
DB 655 CCAGAGAGACGAGTGCATGAGAGTGGCTCTGTAAGTGGTGGCTCAG---TATGGGAG 711
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGlnAsnMetAsnLeuArgThrLeuSer 88
DB 712 CAGCGGCTCTGGAGCTTAAGCTTCATCTGAGGAGAGAGTGGGCTGAGGTCACTGTGC 771
QY 89 GlnLysAlaArgAspAsp----- 94
DB 772 GCCCAAGCCGAGAGAGGGGAGGCCACTCTCCCTCATTTCCCTTACAGCCCAAGTAAACC 831
QY 94 ----- 94

DB 832 CACGTGGGCTCTCCAGCAACCCACTTCACCGCAGTGTCTAAATGCCCTGATCATGAA 891
QY 94 ----- 94
DB 892 TTGCGCGGCGGGGTCACCCAGGGCTCAGAGAGAAGGTTTGAAGACGTGCTGACACA 951
QY 95 -----MetLysLysIleSerGlnAlaMet----- 102
DB 952 TCTGAGCGCGGTGAGAGAAATCTGTCTCACTCTCTTACCAAGCTTTCAGAGCTCC 1011
QY 102 ----- 102
DB 1012 CCAGACCATGATGTCCTCAAGCCAGAGTCAACCAAGCCCCCATTCACAGAGTGTCTG 1071
QY 103 -----GluGlnGluGlyAla--- 107
DB 1072 GGGAGCTGGGGAATCCCACTTCAGCCAGCTTACACCCAGAGAGAGAGGCTCTGGG 1131
QY 108 -----ThrAlaAlaGluThrGluGlu 114
DB 1132 ACCCAATGGCTCTGATGAAAGTCAGAAATTACTACAGAAATCAGAGAAAGAGAG 1191
QY 115 GlnGlnIleSerGlnAlaMetGlnGlnGlnGlyAlaThrAlaAlaGluThrGluGln 124
DB 1192 AGAGAGAAATCAGAGAAAGGAGGAGGCGCCCATGCGCGGTGTGAGAGAGCCCCACAG 1251
QY 135 GlyHisGlyGly----- 138
DB 1252 GCGGCACACGACCTACAGCCCAACCAACCATGGAGGCTTCTGAGAGAGAGCTC 1311
QY 139 ---AspThrTrpAspTrpLysSerHisValMetThr---LysPhe----- 151
DB 1312 TGTTCCATGAGGCTCGAAGAAATGAGATTTTAAACCAAAATTCACACAGCTGCTACTT 1371
QY 152 -----AlaGlnGlnGluAspValArgArgSerPheGluAnThr 164
DB 1372 CTACAAAGACCTACCCAGAGGACAGATGATCCCTGTCTCAAGAGAAC----- 1419
QY 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
DB 1420 -----TGGCTGATTTATGTGAGAGATGAGAGATGAGATTTAATTTAGATCAGAGAC 1470
QY 174 LeuAlaGly---AlaAspSerAspAspTrpGlyPheArgProAlaGlnThrValLeu 192
DB 1471 TTATTTGGCCAGGCTGTGATACCA-----GAACTCTCCATAGTCATCTG 1518
QY 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCySTrpAla 212
DB 1519 CAGGGGCTGTGTGAATGGAGAGTCAACCTGGCCAGGAGGTGAAGAGAAAGCTGGGGG 1578
QY 213 GlnGlyGlyLeuTrpGlnGlyMetPheSerTrpValPhePheLeuProValArgLysMet 232
DB 1579 AGAGCCAGCTGTATGTGGAGACCGCTTCACAGCATGTCTTCACTCAAGCTCAGAGAGCTG 1638
QY 233 GlnArgLysLysGlnSerSerValThrGlnPheIleSerArgLysTrpProAspSerGln 252
DB 1639 GCCACATCCAAAGGTGTGATCTGTGAGCTCATCGAAAGATGGAGAGCCATCCG 1698
QY 253 AlaProValThrGlnIleMetSerArgProGlnArgLeuPheIleIleAspGlyPhe 272
DB 1699 GCTTCCATTAAGACGATCTGTCTAGGCCAGAGGGGTGTCTTCACTTCAGATGGGTGA 1758
QY 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCySLeuAspTrpAlaGlu 291
DB 1759 GATGAGCAGAGATGGGTCTTTCAGAGAGCGAGTTTATAGTCTGTCTGCACTGGAGCAG 1818
QY 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSer 311
DB 1819 CCAAGCGCGGAGTGCATGTGGGAGTTGTGTGGGAAATCAATACTTCCCGAGAGCA 1878
QY 312 PheLeuIleValThrValArgAspValGlyThrGlnLysLeuLysSerGluValSer 331
DB 1879 TCCTTCTGATCAAGGCTGTGAGACACAGCTCTGTGAGAACTCATTTCTTTGGAGCAG 1938

332	ProArgGlyrLeuLeuValAlaArgGlyYLisSerGlyGluIleArgIleHisLeuLeuLeuGlu	351	
Db	1939	GCAGGTGGGTGGAGAGGTCCGGGGGGTCTGTGAGTCCAGCGAAGAAATATTTCTACAGA	1998
Qy	352	ArgGlyIleGlyGluIleHisGlnIleThrcGlnIleuArgAlaIleMetAsnAspGlu	371
Db	1999	TATTTCACAGATTGAAGGCAAGCAATTAGACCTTTAGTTGGTGGTCAATCAAAACAAAG	2058
Qy	372	LeuLeuAspGlnGlyGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu	391
Db	2059	CTCTGGGCGCCCTGTCTGTGGTCCCTGGGTGTCCGGTGGGCTCCAGCTTCGTGATGACG	2118
Qy	392	GlnAspValValGlyGlySerValAlaProPheAsnGlnThrLeuThrGly-----Leu	409
Db	2119	CAGATTGAAGCGGGAAGAAATCACTCACTGATCCCAAGACCAACCAACCCCTGTCTA	2178
Qy	410	HisAlaIaIaPheValPheHisGlnLeuThrProArgGlyValValAlaArgCysValAsn	429
Db	2179	CATTACCTTGCCCAAGCCTCTCCAACTCCAGCATTTGGAA-----	2217
Qy	430	LeuGlnGluArgValValLeuAspArgPheCysAspMetAlaValGlnGlyValTPAsn	449
Db	2218	-----CCCAAGCTCAGAGACCTCGCTGTGGTGGTGGAGGATGTGGCAA	2265
Qy	450	ArgIlySerValPheAspGlyAspAspIleuMetValGlnGlyLeuGlyGlySerGluLeu	469
Db	2266	AAAAAGACCCCTTTCACTCAGTCAAGATGACCTCAGAAAGCATGGGTATGATGGGGCATCATC	2325
Qy	470	ArgAlaIaIaPheHisIleMetAsnIleu-----LeuProAspSerHisCysGlu	485
Db	2326	TCCACCTTCTGAAGATGGGTATCTTCAGAGCACCCAATCCCTCTGAGC-----	2376
Qy	486	GluTrpTrpThrPhePheHisLeuSerLeuGlnAspPheCysAlaIaIaLeuTrpVal	505
Db	2377	-----TACAGCTTCAATTCACCTCTGTTCCAAAGATCTTTGGAGCAATGCTAATGTC	2430
Qy	506	LeuGlnGlyLeuGlu-----IleGluProAlaLeuCysProLeuTrpValGlnIleThr	523
Db	2431	TTGGAGGATGAGGAAGGAGAGATTAACATTTCAATTCATCAATGATTTGGAAAAAGCG	2490
Qy	524	LyAspSerMetGluLeuIleGlnAlaGlyPheHisIleHisSerLeuTrp-----	540
Db	2491	CTAGAAAGCA-----TATGAATACATGGCCGTGTTGGGGCATCA	2529
Qy	541	MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu	560
Db	2530	ACCACACATTTCTATTGGCGCTGTATGATGAGGGGAGAGAGATGGAATGAACATC	2589
Qy	561	LeuGlyCysProValProLeuGlyValIleGlnIleuLeuHisIleTPValSerLeuLeu	580
Db	2590	TTTCACTGCCGGCTGTCTCAGGGCG-----AGAAACCTGAGTCAAGTGGTCCCGTCCCTG	2643
Qy	581	Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys	598
Db	2644	CAGCTGCTGTGCAGCCACAC-----TCTCTGGAGTCCCTCCACCTGC	2685
Qy	599	LeuPheGlnThrGlnAspIleGlnPheValArgLeuAlaLeuAsnSerPheGlnGluVal	618
Db	2686	TTGTACGAGACTCCGGAACAAACCTTCTGTGACACAAATGATGGCCCATTTGAAAGAAATG	2745
Qy	619	TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysValGlnHisCys	638
Db	2746	GGCATGTGTGTGAAGAAACAGACATGAGCTCTTATGTGTGCACCTTCTGTGATTAATTCAGC	2805
Qy	639	ProTrpLeuAspGlyIleArgValAspValIleGlyIlePheProArgAspGlySerAla	658
Db	2806	CGCCACGTCGAGAAACCTTCAGCTG---ATTGAGGGC-----AGCGACACAGATCA	2853
Qy	659	GluAlaIaCysProValValProLeuTrpMetArgAspIleThrLeuIleGlnGlnGluIleTrp	678
Db	2854	ACATGAGCCCAACCAATGGTATCTCTGTTCAAGTGGTGGTCCAGATGACAGAGCCATATGG	2913

QY	679	GIuMrpHeCySvSeMetLeuGIyThrNiSProNiVleuMkGlnLeuMrLeuGIySer	698
Db	2913	-----	2913
QY	699	SeRileuThrGIuArGIaMeuLySThrLeuCyAlaLySeuMkGlnSProThrCyS	718
Db	2913	-----	2913
QY	719	LyvIlleGlnThrLeuMetPheArGIaMnIleGlnIleThrProGIyAlGIlnIleuThrP	738
Db	2914	-----CAGATTCTCTTC	2925
QY	739	ArgIleValMetAlaMnIaArGIaMnLeuArGISeRleuMnIleuGIyThrNiSeuLyS	758
Db	2926	TCGGCTCTTCACAGTCAACGAAACCTGAAGAGACTGAAGCTTAAGTGAACCTGGACG	2985
QY	759	GIuGIuMrValArGISeMetAlaCySeGIuAlaLeuLyvNiSProLySvSeuLeuGIuSer	778
Db	2986	CACCTGCACTGAAGTGAAGACTTTTGTGAACCTTGAAGAGCGGCTCGCTGCTGAGACC	3045
QY	779	LeuArGIleuMrCySvGIyLeuThrNiAlaCySTyTyrLeuLyvIlleSerGlnIleu	798
Db	3046	CTGGCGG-----	3051
QY	799	ThrThrSerProSerLeuLyvSerLeuSerLeuAlaGIyMnLyvAlaThrArGIuGIy	818
Db	3052	-----TTGGCTTGCG-----	3060
QY	819	ValMetProLeuSerArPAlaLeuArGIaValSerGlnCyAlaLeuGlnLyvLeu	838
Db	3060	-----	3060
QY	839	GIuMrCyGIyIleThrAlaThrGIyCySeGlnSerLeuAlaSerAlaLeuValSerAr	858
Db	3061	-----TGTGGCTCAACAGCTGAGAGACTGGAAGAGACTTGTGGCTGAGAGCGAAC	3114
QY	859	ArgSerLeuThrNiAlaLeuCyvLeuSerArMnSerLeuGIyMnGIuGIyAlaArLeu	878
Db	3115	CAGACC-----	3120
QY	879	LeuCyvArGISeMetArGIeupProNiCySerIleuGlnArGISeuMetLeuMnGlnCyS	898
Db	3120	-----	3120
QY	899	HisLeuMrThrAlaGIyCyGIyPheLeuAlaLeuAlaLeuMetGIyMnSerTrpLeu	918
Db	3121	-----CTG	3123
QY	919	ThrNiAlaSerLeuSerMetArMnProValGIuMrMnGIyAlaLyvLeuLeuCyvGIu	938
Db	3124	ACCGAGCTGAGACTGAAGCTTCAAGTGTCTCAGCATCTGAGGCAACACCTTTGGCAG	3183
QY	939	ValMetArGIuProSerCyvNiAlaLeuGlnArMnIleuValLySvCyvNiAlaLeuThr	958
Db	3184	AGACTGAGACAGCGAGCTGCAACCTACAGAGACTGAGCTGGAGCTGTGGCTTACG	3243
QY	959	AlaAlaCySvGIuSerLeuSerCyvAlaIlleSerArGISeRArGIAlaLyvSerLeu	978
Db	3244	TCTGACTCTCTCCAGAGACTGTGCTCTGTGTACTGTCCAGCCCCAGCTGAAGAGACTA	3303
QY	979	ArPLeuThrArPArMnAlaLeuGIyArPArGIyAlaAlaAlaLeuCyvGIuGIyLeuLyS	998
Db	3304	GACCTGAGCAGAAACAACTGGATGACGTTGGCTGGACACTGTCTGTGAAGGGCTCAGG	3363
QY	999	GlnLyvArMnSerValLeuThrArGIeulGIyLeuLyvAlaCyvGIyLeuThrSerArPAr	1018
Db	3364	CATCTGCTCGCAAACTATACGCTGGGGCTGAGCAACAGACAACCTGAAGATGAAGATG	3423
QY	1019	CyvGIuAlaLeuSerLeu-----AlaLeuSerCyvArMnArGIHs	1031
Db	3424	AGGCAAGAACTGAAGGGCCCTGGAGCAGAGAAACCTCAGCTGTCACTTTCAGAGACGG	3483
QY	1032	LeuThrIleSerLeu-----ArPLeuValGIuMnArMnPhe	1042

[illegible]

Db	1337	CTCTGGCCCTGTGTCTTGTGACCTTGGGTGTCCGGCTGGCTGACCTTGGCTATGACG	1596
Qy	392	GlnaPvAlValIglYluserValAlaProPheanGlnThrLeuThrgly-----Leu	409
Db	1597	CAGATGAAGCGAAGAAAACACACATGACACTTCCAAAGACACACACACCTCTGTCTA	1656
Qy	410	HisAlaIaPheValPheHisGlnLeuThrProArgGlyValValAlaArgCyLeuasn	429
Db	1657	CATTACCTTGGCCAGGCTCTCCAAAGCTCAGCGAATTGGAA-----	1695
Qy	430	LeuGlnGluArgValValLeuValArgPheCysArgMetAlaValIglYlValTrpAsn	449
Db	1696	-----CCCCAGCTCAGAGACTCTGTCTCTCTGGCTGTGGTGGGATGGGAA	1743
Qy	450	ArgYlserValPheAspGlyAspAspLeuMetValGlnGlyLeuGlylGlnSerGlu	469
Db	1744	AAAAAGACCTTTTCAGTCCAGATGACCTCAGAAAGCATGGGATTAGATGGGCGATATC	1803
Qy	470	ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu	485
Db	1804	TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCACCCCACTCCCTGAGC-----	1854
Qy	486	GluYrTrpThrPhePheHisLeuSerLeuGlnAspPheCysAlaIaLeuTrpVal	505
Db	1855	-----TACACCTTCATTCACTCTGTGTTCCAAAGATCTTTGACGACATGTCTATGTC	1908
Qy	506	LeuGlnGlyLeuGln-----IleGlnProAlaLeuCysProLeuTrpValIglYlSerThr	523
Db	1909	TTGGAGATGAGAAAGCGAGAGGAAACATCTTAAATTCACATAGATTTGGAAAAGCG	1968
Qy	524	LyAspSerMetGluLeuValGlnAlaGlyPheHisIleHisSerLeuTrp-----	540
Db	1969	CTAGAGACA-----TATGAAATACATATGCGCTGTGGGCGCATCA	2007
Qy	541	MetYsaArgPheLeuPheGlyLeuValSerGlnAspValAlaArgAspProLeuGluValLeu	560
Db	2008	ACCAACACCTTTCCTAATGGCGCTGTAAATATAGATAGGGGAGAGAGATGAGAAACATC	2067
Qy	561	LeuGlyCysProValProLeuGlyValIleGlnIleYsaLeuHisIleTrpValSerLeuLeu	580
Db	2068	TTTCACTGCCCCGCTGTCTCAGGG-----AGAACTGAGGCAAGTGGTCCCCGCTGTG	2122
Qy	581	Gly-----GlnGlnProAsnAlaIleThrThrProGlyAspThrIleAspAlaPheHisCys	598
Db	2122	CAGCTGCTGTCGACGCCACAC-----TCTTGAGTCCCTCCACATGCG	2163
Qy	599	LeuPheGlnThrTrpGlnAspGlyGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal	618
Db	2164	TTGTACGAGACTCGGAAACAAACGTTCTCTGACAAAGTAAAGGCCCATTTGGAAACAAATG	2223
Qy	619	TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnIleCys	638
Db	2224	GGCATGTGTGAGAAACACACATGAGCTCTTAAGTGTCACTTTCTGCAATTAAATTACG	2283
Qy	639	ProTrpLeuAspGlyValLeuArgValAspValYsaGlyIlePheProArgAspGlnSerAla	658
Db	2284	CGCCACGTAAGAAAGCTTCAGCTG---ATTAGGGC-----AGCAGACACAGATCA	2333
Qy	659	GluAlaCysProValValProLeuTrpMetArgAspIleYsaThrLeuIleGlnGlnIleTrp	678
Db	2332	ACATGAGACCCACCATCATGTGTCTCTGTTCAGGTGGGTCCAGTCAACAGATGCGCTAATGG	2391
Qy	679	GluAspPheCysSerMetLeuGlyThrHisIleProHisLeuAspGlnLeuAspLeuGlySer	698
Db	2391	-----	2391
Qy	699	SerIleLeuThrGluArgAlaMetLeuYsaThrLeuCysAlaValYsaArgHisProThrCys	718
Db	2391	-----	2391
Qy	719	LyValIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValIleHisValLeuTrp	738

[illegible]

QY	1069	pcIntYrProValGlnIleArgIlyLeuLeuGlnIleValGlnIleuLeuYrProArGva	1069
DB	3130	-----	3130
QY	1089	IValIleArpOlySerTrpHisSerPheArpGlaArpArghIstlyvIleGlyLeuTh	1109
DB	3131	-----	3138
QY	1109	rPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetArpProG	1129
DB	3139	GATGACTCTTGCGGGCCCAAGGGG-----CTGGCGCACTAGAGGTAGTT	3183
QY	1129	uGlnIlyLeuArgValSerLeuLeuAlaGlyArpPheLeuYSerSerTrpArgPheAla	1149
DB	3184	GACAAAGAAAAG-----ACTGTACCGAGTCACT--	3214
QY	1149	sSerLeuCysLeuAlaThrAlaLeuGlyGluSerGlnArgValArpArvAl--GluGlns	1169
DB	3215	-TCCTCTGAGCTGGCTCTTACCGCTGGCCCAAG--CGGGTCTCTGCTTTGTGTATGGA	3270
QY	1169	eYrSerProGlnProMetAlaGlyThrGlnIstlyvGlnArpIlyMetLeuSerValGly	1188
DB	3271	GAAGCGGTGAC-----CCTGAGATGTAATCTGTGTGTGGAC	3309
QY	1189	--TrpSerGlyAlaTrpSerGlnThrAlaGluGlnGlyLeuGlySerArpSerAla	1208
DB	3310	CAGTTCCTGGGTGAGATCAACCCACACACAGCTGGATGGT--GCCAGGGCTCTGTCTG	3366
QY	1208	srHisArpHisGlyGlyMetAlaTrpSerLeuGlyArgGlyLeuSerSerArgIlyLeu	1228
DB	3367	GACATCA-----GGCTGAGCCTGGAGCTGTGGA--AGCTTGACCTCCCTCACTTT	3417
QY	1228	Yr-----ProThrValLeuMetThrThrAlaValCysProGlyHisTrpGlnArgLeu	1246
DB	3418	GTGGCTCTCCAAAGGG--GCCATGTGACATCTCTGT--TCCAAATGGCCCACTTAA	3473
QY	1246	lySerArgGly-----	1249
DB	3474	AGAGGAGGGAGTGCCTCTGAGAGAAGCCAGGAGGTGAGCTGCATCAATAGTTCTGGA	3533
QY	1249	-----	1249
DB	3534	AAACCCAGCTTCTCCCTTGGAGAGCTCTCTGAATAATGATCAATAATGCCCTGCGCTT	3593
QY	1250	-----TrpCys-----LeuArpSerAlaArpA	1257
DB	3594	CATTCCCGTCACACTGTGTGTGTGTGCTTTACACCGCGTGCATCTGAGAAAGCACCTT	3653
QY	1257	srHisSer-----GlyValSerTrpSerLeuGlyAla	1268
DB	3654	CCACCTCTACCTGATCCCAAGTGAAGTGTCTCATTCGAAAGAACTGGAGC-----T	3704
QY	1268	IaGlyLeuGlnGlyLeuValSerArpSerAlaArpArpHisSerGlyValAla---TrpS	1287
DB	3705	CTGCTATGAAAGCCTTGAGAAAGACACAGCTGTCTCGAGAGTTTACGTGGCCACTGGG	3764
QY	1287	erLeuGlyAlaAla-----GlyLeuGlnGlyLeu	1296
DB	3765	ATCAGAGGATCAAGCTGCAAGTGAAGAACAAGAAAGATGAGACTGTGGTGTGGAGGCTT	3824
QY	1297	-----ValSerArpSerAlaArpArpHisSerGly	1306
DB	3825	GGTGAACCGAGAGATTCATAGCTCGACATCTGATCTCCCTCAAGCCCGCATAGCCGT	3884
QY	1307	-----ValSerTrpSerLeuGlyAlaAlaGlyLeuGlnGlyLeuValSerArpSerAla	1324
DB	3885	ACCTTCACTCTGAGATGCCCGGACAGTTGCTGCACTTGTGTGACACAGATCGAGAGAGCT	3944
QY	1325	ArpArpHisSerGlyValSerTrpSerLeu	1334
DB	3945	GATAGCCCGAGTGAATGG--TGGAGGTGTG	3973

RESULT 7

US-09-388-221B-5

Sequence 5, Application US/09388221B

Patent No. 6818750

GENERAL INFORMATION:

APPLICANT: Reed, John C.

TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation

FILE REFERENCE: P-1J 3650

CURRENT APPLICATION NUMBER: US/09/388,221B

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 4332

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(4332)

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QY 1137 uAlaGlyAspPheYsSerSerThrArgPheAlaYsSerLeuYsLeuAlaThrAlaAs 1157
DB 3672 CCCAGCGAC-----GCTTGTAAACAAAGCGATAGA 3704
QY 1157 nGlyYsSerGlnArgValAspAsnValGlnGlnSerSerProGlnProMetAla---- 1175
DB 3705 TGATAGAGAAAGATCCCTTCATGCTGTGTGGCTGACAGCTTGGCCCAATGAACCT 3764
QY 1176 ----GlyThrGlnHis-----LysGln 1181
DB 3765 GAACTTTGCTTCACTTATTATTGTCTATTCTGTACTAAGTGAAGTAAATGCCAAGA 3824
QY 1181 nAspYsMet-----LeuSerValGlyYrSerGln 1191
DB 3825 GTTGAAATTTGCTCAAGAGCCCTGAGAAATTCAGACCTTCAAAATTCATAGCTGG 3884
QY 1191 yAlaTrpSerGlnThrAlaGlnLeuGlnGlyLeuGlySerAsnSerAlaAspHisAspHis 1211
DB 3885 GCAAGATGAAGAAACCATTCACCTTGAG-----ATTACTGAAAAAAGACA 3929
QY 1211 sGlyYsMetAlaTrpSerLeuGlnYsArgGlnLeuSerSerArgGlyLeuYs----- 1228
DB 3930 TGGAGCTTTGCTGTGGATACGA-CGTGAAGCCATGATCTCCAGCTTTAGCTGAT 3988
QY 1229 ----ProThrValLeuMetThrThrAlaValCysProGly 1240
DB 3989 CAGCCCTCTCTCTTCTCAAGGTGAGCCTTGTGAAGA 4028

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RESULT 9
US-09-388-221B-9
; Sequence 9, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4365)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-9
Alignment Scores:
Pred. No.: 2,84e-84 Length: 4556
Score: 945.50 Matches: 363
Percent Similarity: 37.97% Conservative: 208
Best Local Similarity: 24.14% Mismatches: 525
Query Match: 13.37% Indels: 410
DB: 3 Gaps: 47
US-10-066-521-6 (1-1344) x US-09-388-221B-9 (1-4556)
QY 11 SerYrGlyLeuGlnTrpCysLeuYrGlu--LeuAspYsGlnGlnPheGlnThrPhe 29
DB 13 GCTTCTGCTGCGCATTAAGCGCATCTCAAGAGCTTTGGGGTGAACACCGCTCAG 72
QY 30 YsGlnLeuLeuYsYsYsSer--SerGlnSerThrThrCysSerIleProGlnPhe 48
DB 73 CAGCTTCTGCTGCGCATTAAGCGCATCTCAAGAGCTTTGGGGTGAACACCGCTCAG 132
QY 49 GlnIleGlnAlaAsnValGlnCysLeuAlaLeuLeuHisGlnYrYrGlyAla 68
DB 133 CCAAGAAAGACAGTGGCATGAGTGGCTCTGATACCTGTGGTGCAG--TATGGGAG 189
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGlnAsnMetAsnLeuYrThrLeuSer 88
DB 190 CAGCGGCTGGAGCTTACCTTCCATACCTGGAGCAGATGGGCTGAGTCACTGTGC 249
QY 89 GlnYsAlaArgAspAsp----- 94
DB 250 GCCAAAGCCAGAAAGGGCAGGCCCATCTCCCTCATTTCCCTTACAGCCCAAGTAAACC 309
QY 94 ----- 94
DB 310 CACTGGGGTCTCCAGCCAAACCACTTCACCGGAGTGTAAATGCCGTGATTCATGA 369
QY 94 ----- 94
DB 370 TTGCGGCGGGGTGACCCAGAGGCTCAGAGAAAGGTTTGAAGACAGCTGCTGACACA 429
QY 95 -----MetYsYsIleSerGlnIleMet----- 102
DB 430 TCTGAGACCGCTGAGAGAAATCTCTGCTTCACTCTTACCAAGCTTTTCAAGCTTC 489
QY 102 ----- 102
DB 490 CCAAGACATGATCTCCAAAGCAAGAGATCAACCAAGCCCAATCCACAGCAAGTGTG 549
QY 103 -----GlnGlnGlnYsAla-- 107
DB 550 GGAAGCTGGAGATCCCACTTACGCCCAAGCTTACAGCCCAAGAGAGAGGCTCTGGG 609

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QY 108 -----ThrAlaIaIaGluThrGlu 114
DB 610 ACCCAATGGCTCTGATGAAGCTCAGAAATTACTACACAGAAATCAGAAAGAG 669
QY 115 GlnGluIleSerGlnAlaMetGluGlnGluValAlaThrAlaAlaGluThrGluGln 134
DB 670 AGAAGAAATCAGAAAGGAGAGCCGCCATGCGGACGCGGTGAGGAGCGCCGCCAG 729
QY 135 GlyHisGlyGly----- 138
DB 730 GCCGACCAAGCTCAGCCCAACCAACCCATGGAGCCTTCTGTGAGAGAGCCTC 789
QY 139 ---AspThrTrpAspTyrIleSerHisValMetThr---LysPhe----- 151
DB 790 TGTTCACATGGCCCTGAAAAATGAGATTTTAAACAAAATTCAACAGCTGCTACTT 849
QY 152 -----AlaGluGluGluAspValAlaArgAspSerPheGluAsnThr 164
DB 850 CTACAAAGACCTCAGCCCAAGAGCCAGATCCCTGCTCAAGAGAAC----- 897
QY 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
DB 898 -----TGGCTGATTATGTCAGAGAAATCAGAGACATTAAATTGAGATCAGAC 948
QY 174 LeuAlaGly---AlaPheAspSerAspArgTyrGlyPheArgProArgThrValVal 192
DB 949 TTATTTGGCCCAAGCTCGATACCA-----GAACTCCGATATGATCATCTG 996
QY 193 HisGlyIleSerGlyIleGlyIleSerAlaLeuAlaArgArgIleValLeuCySerTrpAla 212
DB 997 CAGGGGCTCTCGAATTTGGAACTCAACTGGCCAGCGAGGAGAAAGCCTGGGG 1056
QY 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
DB 1057 AGAGCCAGCTGTTATGGGAGACCGCTTCAGATCTTTTACTTCACTGACGTGAGAGCTG 1116
QY 233 GlnArgIleIleSerGlyIleValPheIleSerArgIleTrpProAspSerGln 252
DB 1117 GCCCAGTCCAAAGGAGTGTCTGTCAGCTCATCGAAAAAGTGGAGCCAGCTCCG 1176
QY 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGlyPhe 272
DB 1177 GCTCCCATAGACATCTGTCTAGGACAGAGCGCTGCTTCATCTCGATGAGGTGA 1236
QY 273 AspAspLeuIleSerValIleLeuAsnAsn---AspThrIleLeuCySerValAspTrpAlaGlu 291
DB 1237 GATGAGCCAGATGGGCTTTCAGAGCCAGATTTCTAGCTGTGTCTGCACTGGAGCCAG 1296
QY 292 LysGlnProPheThrLeuIleArgSerLeuLeuArgValLeuLeuProGluSer 311
DB 1297 CCACAGCCGCGCATGACGTCTGGGCACTTGTGGGAAAAATATATATCTCCGAGGCA 1356
QY 312 PheLeuIleValThrValArgAspValGlyThrGluIleLeuIleValSer 331
DB 1357 TCCCTCTGATCAGCGCTCGGACCAAGCTCTGCAAGAACCTCATCTCTTCTTGGAGCAG 1416
QY 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluIleArgIleHisLeuLeuLeuGlu 351
DB 1417 GCAGTGTGGGTAGAGGTCTGGGGTCTCTGAGTCCAGCAAGAAATATTTTACAGA 1476
QY 352 ArgGlyIleGlyIleHisGlnIleValThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
DB 1477 TATTTCACAGATGAAGGCAAGCAATTAGAGCTTTAGGTTGTCATTAACAAGAG 1536
QY 372 LeuLeuAspGlnCySerGlnValProAlaValGlySerLeuIleCySerValAlaLeuGlnLeu 391
DB 1537 CTCCTGGCCCTGTGTCTTGTGCTCTGGGTGTCTGCTGGCTGCACCTTGTGATGACAG 1596
QY 392 GlnAspValValGlyIleSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409
DB 1597 CAGATGAAGCGGAAAGAAAATCACTACATGACTTCAGAGACCAACCAACCTCTGTGCTA 1656

QY 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValAlaArgArgCySerLeuAsn 429
DB 1657 CATTACCTTGGCCAGGCTCTCAAGCTCAGCCATTGGGA----- 1695
QY 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449
DB 1696 -----CCCAAGCTCAGAGACCTGTCTCTGCTGTGAGGAGCATCTGGCA 1743
QY 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyIleSerGluLeu 469
DB 1744 AAAAAGACCTTTTCACTGCATGACATGACCTCAGAAAGATGGATTAGTGGGCATCATC 1803
QY 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCySerGlu 485
DB 1804 TCCACCTTCTTGAAGATGGGTATTTTCAAGACACCCCATCCCTGTGAC----- 1854
QY 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaIleLeuTyrTyrVal 505
DB 1855 -----TACAGCTTCATTCACCTCTGTTCAGAGAGTCTTTGACGAAATGCTCTATGTC 1908
QY 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCySerProLeuTyrValGluIleThr 523
DB 1909 TTGAGAGATGAGAAAGGAGAGGTAAACATTTAATTGATCATATGATTGAAAAAGACG 1968
QY 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
DB 1969 CTAGAAGCA-----TATGAAATATACATGAGCTGTGTGGGCATCA 2007
QY 541 MetLysArgPheLeuPheGlyLeuValSerGlnAspValAlaArgArgProLeuGluValLeu 560
DB 2008 ACCACACGTTTCTTATGGCCTGTATGATGAGGAGGAGAGAGATGAGAAACATC 2067
QY 561 LeuGlyCySerProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
DB 2068 TTTCACGTCCGGGCTGTCTAGGGG-----AGAACTGATGACATGAGTCCGCTCCCTG 2121
QY 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCySer 598
DB 2122 CAGCTGTCTGAGCCAC-----TCTGTGAGCTCTTCCACTGTC 2163
QY 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
DB 2164 TTGTACAGACTGGCAACAAACGTTCTTACACAACTATGCGCCATTTTGGAAAGATG 2223
QY 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCySerGlnHisCySer 638
DB 2224 GGCATGTGTAGAAACAGACATGAGCTCTTGTGTGTCATTTCTGCATTAATTCAGC 2283
QY 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProAlaArgArgIleSerAla 658
DB 2284 CGCCACGTGAAGAGCTTCAGCTG--ATTGAGGGC-----AGCAGCAACAGATCA 2331
QY 659 GlnAlaCySerProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678
DB 2332 ACATGAGCCCAACATGTATGTCCTTCAAGTGGGTCCCACTGACAGATGCTATTTGG 2391
QY 679 GluAspPheCySerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
DB 2391 ----- 2391
QY 699 SerIleLeuThrGluArgAlaMetLysThrLeuCyAlaLysLeuArgHisProThrCys 718
DB 2391 ----- 2391
QY 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738
DB 2392 -----CAGATTCTCTTC 2403
QY 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeuLys 758
DB 2404 TCGTCTCAAGTCAACAAACCTGAGAGAGCTGACCTAAGTGAACCTGCTGAGC 2463
QY 759 GlnGluAspValArgMetAlaCySerGluAlaLeuLysHisProLysCySerLeuLeuGluSer 778

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Db      2464 CACTCTGCAAGTAAGAGCTTTGTAAGACCTGAGAGACCTCGCTGCTCTGAGAGACC 2523
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      779 LeuArgLeuArgCyCyGlyLeuThrHisAlaCysTyrLeuLeuValIleSerGlnIleLeu 798
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2524 CTGGGGTGGGCTGGCTGGCTGCTCAAGCTGAGAGCTGCAAGAGACCTTTGGGGCTG 2583
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      799 ThrThrSerProSerLeuLeuSerLeuSerLeuValGlyLeuValIleThrAspGlnGly 818
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2584 AGAGCCACCAAGACCTGAGCTGAGCTGAGCTTCAATGCTCAAGAGAGTCTGGA 2643
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnIleLeu 838
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2644 GCCAAACACCTTTCGACAGACTGAGACAGCGAGCTCAAGCTACAGAGCTGAGCTG 2703
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      839 GluArgCyGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2704 GTCAAGCTGGCTCCTCACTGACTGCTGCTGAGAGACCTGGCTGCTTGAAGTCCAGC 2763
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeu 878
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2764 CCCAGCTGAAAGAGCTTACCTGACAGAGAACCACTGAGATGACCTTGGGGCTGAGACTG 2823
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      879 LeuCyArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2824 CTCTGTGAGGGGGCTCAGGCACTCTGCTGCTGCAAACTCATACGCTGGGGCTGAGACAGACA 2883
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      899 HisLeuAsp----- 901
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2884 ACTCTGATGATGATGATGAGGAGAGAGACTGAGGGCTTGAAGAGAGAAACCTGAGCTG 2943
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      902 -----ThrAlaGlyCysGlyPheLeu 908
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2944 CTCAATCTTCACAGACGAGAAACCAAGTGTATGACCCCTTACTGAGGGC-----CTG 2994
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      909 AlaLeuAlaLeuMetGlyAsnSerTrp-----LeuThrHisLeuSerLeu----- 923
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      2995 GATACGGGAGAGATGATGATGATGACATCTTCATCTCAAGCGGACAGAGCTGGATCAGAG 3054
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      924 ---SerMetAsnProValGluAspAsnGlyValIleLeuLeu----- 936
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3055 AGGGCGGCTCCCATGTTGCTCAGCGCTATCTCAAACTCTGAGAGCTGAGAGAGATCTTTC 3114
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      937 -----CysGluValMetArgGluProSerCysHisLeuGlnAspLeuGlnValIle 954
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3115 CCAATTGCTGAGATTGACAGAGAAAGCTCCCAAGAGTATGACCGGTGGAACCTTGTGC 3174
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      954 sCys-----HisLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSerArg 971
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3175 GTGCTCTCTCTGCTCTCAAGGGGAGCTGCTATGAGAGCTTTGGGAGCTGAGATGAC 3234
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      971 gSerArgHisLeuIleuIleuSerLeuAspLeu-----ThrAspAs 983
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3235 TTTCTGGGGCTTGAAGAAATGTGATGTGATGATTGATTGATTAAGAGACAACAACAGATAC 3294
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      983 nAlaLeuGlyAspGlyValAlaAlaLeuCysGlu----- 995
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3295 AGCGTTTGTTCCTCCCACTGCTGGCTGCTGATCTGTGTGCTGAGCCAGCAGCGCTGGCTTCTG 3354
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      996 -----GlyLeuIleuValIleuValIleuValIleuValIleuValIleuValIleu 1014
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3355 GTAAGGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 3414
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1014 uThrSerArgCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSe 1034
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3415 GACCTGCAAGCAACATGAAACAGTGGCTGTGGCGGCCCTTGTGATGTCACTCAGAG 3474
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1034 rLeuAsnLeuValGlnAsnAsnPheSerProIleGlyMetMetIleValCysSer----- 1052
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3475 C-----CAGAGAGGCTGTGCGCGAAATCCACCTCCCACTTCACTTCCCTC 3522
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1053 -----AlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu-----TrpIly 1068
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...

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Db      3523 CAGGTGAGTGAAGCTCTCTGCTGCTTCTCTGCTGCCCATTTTAAAGATGAAGGATGCTC 3582
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1068 sTrpGlnIleProValGlnIleArgIleLeuLeuGlnIleValGlnIleLeuIleuIleuProAr 1088
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3583 CTGAGG-CATCAAGCCCGGGGAGAGCCTTTTATGCTGTCTGAAA-----AGCCCAAG 3635
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1088 gValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHisIleValIleGlyLe 1108
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3636 CTCTCTCTGATGGGCACTCTGCTGGGATGCGCAGTGGAGACTGCGCTCTCATCTCCCAT 3695
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1108 uThrPheArgLeuProGlnSerArgAlaTrpProCysAlaLeuLeuThrProGlyMetAsnPr 1128
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3696 CACTTCCAAAC-----ACATGTATCTATTTATCAACCCCAACC 3731
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1128 oGluGln---LysIleArgValSerLeuLeuAlaGlyAspPheIleSerSerThrArgPh 1147
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3732 GAAAGATTTAAAGTTTCCACTTGTACTTGTCTCCAGCAGAC----- 3771
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1147 eAlaIleSerLeuCysLeuAlaThrAlaAsnGlyGlnSerGlnArgValAspAsnValGln 1167
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3772 -----GCTTGTCTAAACAAAGCGATGATGATGATGAGAGAGATGCTTCATGTGTGCG 3824
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1167 uGlnSerSerProGlnProMetAla-----GlyThrGlnHis----- 1179
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3825 CTGCAAGCTTCCGCCCCCAATGGAACCCCTGAACCTTGTGCTTCCAGTTATATGTGTGTA 3884
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1180 -----LysGlnAspIleMet----- 1184
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3885 TTCTGCTAAGCTGAAAGATATGCCCAAGAGATGTAATTTGCTTACAGAGACCCCTGAGAG 3944
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1185 -----LeuSerValGlyTyrSerGlyAlaTrpSerGlnThrAlaGlnLeuGlnGln 1201
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      3945 AATTACAGACTTCTCAAAATTTCTATGTGTGGCAGATGAAGAAACCATTTCAACTGAG-- 4002
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1201 yLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArgGln 1221
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      4003 -----ATTACTGAAAAAAGACATGGAGCTTGTGTGTGGATGACTGA-GGTGA 4048
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1221 uLeuSerSerArgGlyLeuCys-----ProThrValLeuMetThrThrAlaVal 1237
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      4049 AGCCAGTGATGATCTCCAGCTTGTAGCTGCATGACGCCCTTCTCTTCTCAGGTGAGGCT 4108
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Qy      1237 lCysProGly 1240
      |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db      4109 TTGTGAAGGA 4118
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RESULT 10
US-10-183-770A-1
; Sequence 1, Application US/10183770A
; Patent No. 6949363
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE REFERENCE: D0067A CIP
; CURRENT APPLICATION NUMBER: US/10/183,770A
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/257,773
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 10/028,374
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4931
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1320)..(2666)
US-10-183-770A-1
Alignment Scores:

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Pred. No.:	1.02e-80	4931
Score:	911.00	352
Percent Similarity:	39.904	189
Best Local Similarity:	25.964	469
Query Match:	12.884	Indels: 351
DB:	3	Gaps: 43

US-10-066-521-6 (1-1344) X US-10-183-770A-1 (1-4931)

[illegible]

QY	322	ThrGlnIysLeuLysSerGlnValValSerProArgTrpLeuLeuValArgGlyIleSer	341
Db	1556	TTGAGAAAGCTCCACCGCTCTGTGGACACCCGACGATGTGAGATCTGGGCTTCTCT	1655
QY	342	GlyGlnGlnArgIleHisValLeuLeuGlnArgGlyIleGlyGlnHisGlnLysThrGln	361
Db	1656	GAGCGCAAAAGAGAGAAATCTTCTTCAAGATTTTCCAAATGACAGACGAGCGGCCCA	1715
QY	362	GlyLeuThrArgAlaIleMetAsnAsnArgGlyLeuLeuThrArgGlnGlnValProAlaVal	381
Db	1716	GTCTTCAATTACGTGAGGAGACACAGACCTCTCTTCCACATGTCTTCTGCTCCCTGATG	1775
QY	382	GlySerLeuIleCysValAlaIleGlnGlnLeuAspValValGlyGlnSerValAlaPro	401
Db	1776	TGCTGGGAGTGTTGATCTGCTGCTCCAGACAGACGTGAGGGGTGGGCTGTGTGACAG	1835
QY	402	PheAsnGlnThrPheThrGlyLeuHisValAlaIlePheValPheHisGlnLeuThrProAla	421
Db	1836	ACGTTCAGACACCACTGACAGTGTACCTGTACTCTGCTGAGTCTGTATCCAAACCAAG	1895
QY	422	GlyValValAlaArgArgCysValLeuAsnLeuGlnGlnArgValValLeuLysValArgPheCysArg	441
Db	1896	CGGGGGGCGCGCGCC-----CTCCAGCGCCCAACCCAGACGAGGGGTGTGTCTCC	1946
QY	442	MetAlaValGlnGlyValTyrAsnArgLysSerValPheAspGlyAspArgLeuMetVal	461
Db	1947	TTGGCGGCGAGATGGGCTCTGTGAAATCAGAAATCTTATTGAGAGCAAGACCTCCGAAG	2006
QY	462	GlnGlyLeuGlyGlnSerGlnLeuArgAlaLeuPheHisIleMetAsnIleLeuLeuProArg	481
Db	2007	CAGCGCTTACAGCGGGAGAAAGACTCTGTGCTCTTCTTCCAAATGAATCTTCCAAAGAGAC	2066
QY	482	SerHisCysGlnGlnIuTyrTyrThrPhePheHisIleLeuSerLeuGlnAspPheCysAlaIle	501
Db	2067	ATCAACTGTGAGAGG-----AGCTTCTGTGCACATCCAC-----	2099
QY	502	LeuTyrTyrValIleGlnGlyLeuGlnIleGlnProAlaLeuCysProLeuTyrValGln	521
Db	2099	-----	2099
QY	522	LysThrLysArgSerMetGlnLeuLysGlnAlaGlyPheHisIleHisSerLeuTrpMet	541
Db	2099	-----	2099
QY	542	LysArgPheLeuPheGlyLeuValSerGlnAspValArgArgProLeuGlnValLeuLeu	561
Db	2100	AGCGGCTTCTGTTTGAAGCTCTTCAACAGAGAGACAGAGACCCCTGGAAAGAGATCTC	2159
QY	562	GlyCysProValProLeuGlyValLysGlnLysValLeuHisIleTrpValSerLeuLeuGly	581
Db	2160	TGCTGGAAAGTCTGGCGGACATCAATGAGACCTGTGGACGTGATGATCAAAAGAAAGCT	2219
QY	582	GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysValPheGln	601
Db	2220	CAGAGCGACGGCTCCACCTTCAGACAGGGCTCTGTGAGTCTTTCAGCTGCTTGTACAG	2279
QY	602	ThrGlnAspLysGlnPheValArgLeuAlaLeuAsnSerPheGlnGlnValTyrProAla	621
Db	2280	ATCCAGGAGAGAGAGTTTATCCAGAGAGCCCTTGAACACTTCCAGTGATGTGTGTACGC	2339
QY	622	---IleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysValGlnHisCysProTyr	640
Db	2340	AACATGTGCTCCAAAGATGAGACATAGGTCTCTCTGTTCTGTGAGAGCGCTGACAGAC	2399
QY	641	LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGlnSerAlaGlnAla	660
Db	2400	GCCCAAGGTGCTGACCTGTATGAGCGCACTTACAGCGCGAGCGGGAGAAAGCCGGCGAGG	2459
QY	661	CysPro-----ValValProLeuTrpMetArgAspLysTyr---LeuIleGln	675
Db	2460	TGCTCCGAGAGAGCGACACAGCTGTGTGTGTGACGCTACAGAGAGAGACCGTTCTGTCTGAC	2519
QY	676	GlnGlnTrpGlnAspPheCysSerMetLeuGlyThrHisProHisValArgGlnLeuAsp	695


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Db      2520 GCCTACAGTGAACATCTGGACGGCCCTGTGGACCAATCCAACTGTATAGACTGTCT 2579
Qy      696 LeuGlySerSerIleuThrGluArgAlaMetCysThrLeuCyValAlaLeuArgHis 715
Db      2580 CTGTACCGAATATGCTGGGCGAGCCGGGGGTGAAGCTGCTCTTCAGAGACTGACAGAC 2639
Qy      716 ProThrCysValIleGlnThrLeuMetCysPheArgSerAlaGlnIleThrProGlyValGln 735
Db      2640 CCCAACTGCACAACTTCAGAACCTTGAAGTAAATTTATCATATATACATGATATTGTA 2699
Qy      736 ---HisLeu---TyrArgIleValMetAlaAsnArgAsnLeuArgSerLeuMetLeuGly 754
Db      2700 ATAATATATTGGCAGGTATGATGCTCAGGCC---TGTAAATCCAGACACTTGGAGG 2756
Qy      754 Y-----ThrHisLeuGlyGluGluAspValArgMetAlaCysGluAlaLeu 770
Db      2757 CCCAGATGGGAGGATCATTGACCCAGAGATTCAAGACAGCTGCGCAACATGGTGA 2816
Qy      770 HisProLysCysLeuLeuGluSerLeuArgLeuAspCysGlyLeuThrHisAlaCy 790
Db      2817 ACC-CGATCTCTACTAA-AATACC----- 2839
Qy      790 sTyrlLeuYsIleSerGlnIle-----LeuThrThrSerProSerLeuLysSerIle 807
Db      2840 -----AAATGAGCCAGGAGATGGTGACACAGCTCTTAAGCCAGCTACTCAGAGAGC 2892
Qy      807 uSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuAr 827
Db      2893 CAAGCAGAGAGG----- 2905
Qy      827 gValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGl 847
Db      2906 -TTCTTCAACCCAGAGCAGAGAGGTGTGGCTGAAGAGGTGCCGCACTCCAGCTCAGC 2964
Qy      847 YCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCyLeuSe 867
Db      2965 CTGGAGAGACCTCTCTGAGCTCATAGCCAAATGAAATTTGACAAGATGAGATCTCAG 3024
Qy      867 rAsnAsnSerLeuGluYasnGluGlyValAsnLeuLeuCyArgSerMetAlaGluProH 887
Db      3025 TGGCAACGCGCTTGATTCACAGGATGATGCTGTTGGCAGGGCTGGCCGATCCCA 3084
Qy      887 sCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPh 907
Db      3085 ATGCAAGCTGCAGATGATTCAGTTGAGAGAGTGAAGTCCGGGGCTGTGCAGCA 3144
Qy      907 eLeuAlaLeuAlaLeuMetGlyAsnSerTyrLeuThrHisLeuSerLeuSerMetAsnPr 927
Db      3145 GATGCTCTGTGCTTGGCAGCAACCAACCATCTGTGATGAGTTGACCTGACAGAAATGC 3204
Qy      927 oValGluAspAsnGlyValLysLeuLeuCyGluValMetArgGluProSerCysHisLe 947
Db      3205 ACTGAGAGATTTGGGCTGAGGTTACTATGCGCAGGAGCTGAGGAGCCAGTGTGAGACT 3264
Qy      947 uGlnAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCy 967
Db      3265 ACGGACTTTGGCTGGAAGATCTGCAGCTCACTGCTGCTGTGACGAGACTGGCTC 3324
Qy      967 sValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAlaAlaLeuGlyAs 987
Db      3325 AACTCTCAGTGTGAACCAAGAGCTGAGAGAGTGAAGCTGAGCTGAGAGTGGGGA 3384
Qy      987 pGlyValAlaAlaAlaLeuCyGluGlyLeuLysGlnLysAsnSerValLeuThrArgLe 1007
Db      3385 CCTGGGGGTGCTGCTGTGTGAGGGCTCAGGATCCCAAGTCAAGCTTCAGACCT 3444
Qy      1007 U-----GlyLeuLysAlaCyGlyLe 1014
Db      3445 GCGGTAGTCCCGTTTGTCTACCAAGCTGAGAGTCCCAATCAGTAAGAGCA---GCCCT 3501
Qy      1014 uThrSerAspCysGluAlaA---LeuSerLeuAlaLeuSerCyAsnArgHisLeuTh 1033

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Db      3502 CTCACCTGGAGCACAGGAGCCAGTTGTCTGTGCTCTTAACCTAGTACTACATCAG 3561
Qy      1033 rSer----- 1034
Db      3562 CCTTTTATTTTATTTTGTGAGACTCCCAAGTACTGATATACAGGCCGCCGCCACCA 3621
Qy      1035 -----LeuAsnLeuValGlnAsnAsnPh-----SerProLysGly 1046
Db      3622 GCCAGCAATTTTGTGATTTTGTAGAGACAGGGTTTCATCATGTATGACAG-GATGG 3680
Qy      1046 YMetCysLeuLeuCySerSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLe 1066
Db      3681 TCTCATCTTCTGACCTTCATGATCTGCTGC-----CTTGAGCT 3719
Qy      1066 uTyrLys---TyrGlnTyrProValGlnIleArgLysLeuLeuGluValGlnLeu 1085
Db      3720 CCCAAAGTCTGGGATTTAC-----AGCTTGAGCCACTGACCCAGCTTACATCAGCT 3773
Qy      1085 uLysProArgValAlaIleAspGlySerTyrHisSerPheAspGluAspAspArgHisLys 1105
Db      3774 TTTTAAAGATTTTCTGCGCGG-----CATGGTGGCTGACACCT 3815
Qy      1105 sIleGlyLeuThrPheArgLeuProGluSerArgAlaTyrProCysAlaLeuLeuTyrGl 1125
Db      3816 TAATTCAGCAGCTTTTGGAGGCGGAG-----TGGAGGATCAGCTGAGGTGGG 3866
Qy      1125 YMet-----AsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysE 1143
Db      3867 AATTGAGACCAAGCTTACCAACATGTGAAGAACCCCATTTGTACTTAAATTCAAAG 3926
Qy      1143 rSerThrArgPheAlaLysSerLeuCyLeuAlaThrAlaAsnGlyLeuSerGlnArgVal 1163
Db      3927 TAGCAGGAGCATG---TGTGCATGCCATATATACAGCTACTCGGAGGCTGAGGAGCAG 3983
Qy      1163 lAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluHisLysGlnAspLy 1183
Db      3984 AGAATCCCTTGAA----- 3996
Qy      1183 sMetLeuSerValGlyTyrSerGlyAlaTyrSerGluThr---AlaGluLeuGluLysLe 1202
Db      3997 -----CCGGAGGTGAAGTGTGCTGTGAGCTGATGAGTGCACCTT 4037
Qy      1202 uGlySerAsn-----SerAlaAspHisAspHisGlyLys 1214
Db      4038 GCATCCAGTGTGGGCAACAAGAGGAAATCCGCTCAAAAAAAGAGGGGGGCTT 4097
Qy      1214 cAlaTyrSerLeuGluArgLysLeuSerSerArgGlyLeuCyAspProThr----- 1230
Db      4098 TTCT-----GAGGACGGCC-CTTGGCAACAGCAATCTTATTC 4135
Qy      1231 -----ValLeuMetThrThrAlaValCyAspProGlyHisTyrGlu----- 1243
Db      4136 CTGGCAGTCCCTTGTGCTGTGTCCTCTTGGCTGTGAAGATTCATTTTCTTCTG 4195
Qy      1244 -----ArgLeuGlySerArgLys----- 1249
Db      4196 AACACTTTTACTTTGATTTTGAAGACAGGCTTGTGCTGTACCAAGTGTGGAGTGA 4255
Qy      1250 -TyrCysLeuAsnSerAlaAspAspHisSerGlyValSerTyrSer 1264
Db      4256 GTGGGT-----GATCATAGCCCGACATCTGGGCT 4286

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RESULT 11

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US-10-781-294-17
; Sequence 17, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowksi, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia

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Qy 572 yslleuLeuH1strValSerleuLeuGlyGln-----GlnProAsnLat 587
Db 1721 AGCCCTGCGGTGGTGCAGGAGCAAGGAGGCTGCCCGAGTGCACCAAGGTGA 1780
Qy 587 hr-----T 588
Db 1781 CCGAGGGGGGCGCAAGGCTGCAGGACACCGAAGGCCAGAGAGGAGGAGGAGAGG 1840
Qy 588 hrProGlyAserThrLeuAspAlaPheH1sCyLeuPheGlnThrGlnAspGlyLeuPheV 608
Db 1841 AGCCCACTACCCCACTGAGAGTGGCTGACTCTCTGTACAGACGAGAGGACCGCTTTG 1900
Qy 608 alaArgLeuAlaLeuAsnSerPheGlnGlnValThrLeuProIleAsnGln-----AsnI 626
Db 1901 TGCCTCCAGGCTCTGCGCGGTCCCGAGCTGGCGGCTGCAGAGAGTGCCTTTCGCCCA 1960
Qy 626 euAAspLeuIleAlaSerSerPheCyLeuGlnH1sCyProTyLeuArgIysIleArgV 646
Db 1961 TGCAGCTGGCTGTCTAGCTACTGCTGAGAGTGTCTGCTGCTGCAGAGGACCTGCGGC 2020
Qy 646 alaAspValIysGlyIle-----PheProArgAspGlnSerAlaGluAlaIac 661
Db 2021 T-GATTCAGCTCAGATTTGTTGCTGCAGGAGAAAGAAAGAGAGCTGCGGAGGCG 2079
Qy 661 ysrProValProLeuThrMetArg-----AspGlyThrLeuLeuGlnGlnT 678
Db 2080 CTCGAGGCGGACCTGGGTGGCGGAGCTGGCGGAGCCCAACTGC--CTCCAGAAATACC 2138
Qy 678 rpgIAspPheCySerMetLeuGlyThrH1sProH1sLeuArgGlnLeuAspLeuGlyS 698
Db 2139 CTTTCGACCACTCTGCTGACATCTGCC---CACAACCTTCCACAG--ACCTTCGGCT 2192
Qy 698 erser-----IleLeuThrGlnArgAlaMetIysThrIleuCyAlaIysLeuArgH 715
Db 2193 CCTCCAGGCGAAGGCTTTGCCAGAG-----TTCCCTTGAAATATAGCTCCCAAT 2240
Qy 715 isProThrCyLeuIleGlnThrIleuMetPheArgAsnAlaGlnIleThrProGlyValG 735
Db 2241 TCAGCCCTGC-----CCAGGGGCTT 2261
Qy 735 InH1sLeuTrpArgIleValMetAlaAsnArgAsnLeuAspSerLeuAsnLeuGlyIy 754
Db 2262 GGCATCTTTGAGAGGATGAATG---TCACGGTGTGGCAGGGGCTGGCCCTCCAGGAC-C 2317
Qy 755 -----ThrH1sLeuIysGlnGluAspValArgMetAlaCyGlnIleAlaLeuIsh1sProL 773
Db 2318 CAAGAGCCAT-----GCAATGACTGACCCAC 2344
Qy 773 ysrCyLeuLeuGlnSerLeuArgLeuAspCyysGlyLeuThrH1sAlaCystrIleuL 793
Db 2345 TGTGTCATCTGAGCGCTCAGCTGCCTCCACTGCAATCCCTGACCGGTCTGCCGAG 2404
Qy 793 yslIleSerGlnIleLeuThrThrSerProSerLeuIysSerLeuSerLeuAlaIysAnL 813
Db 2405 ACCTTTCTGAGGCCCTGAGGGGAGGCCCGGCACTACGAGAGTGGGCTCTCCCAACA 2464
Qy 813 ysrValThrAspGlnIyValMetProLeuSerAspAlaLeuArgIysSerGlnCyAlaAl 833
Db 2465 GGCCTCAGGAGGAGGAGGAGCTGAGTGTAGAGGAGGCTGAGCGCGGAGTGCAGGG 2524
Qy 833 euGln-----LysLeuIleLeuGlnAspCyysGlyIleThrAlaThrIyCyysGlnSerL 851
Db 2525 TGCAGACGCTGAGGCTGACGCTGCCTGAC-----CCCGAGGAGGCTCCCAATACC 2575
Qy 851 euAlaSerAlaLeuValSerAsnArgSerLeuThrH1sLeuCyAspSerAsnAsnSerL 871
Db 2576 TGTGAGGATGTTTGGCAGAGCCCTGCCCTTACCACTGATCTCAGCGGCTGCCAAC 2635
Qy 871 euGlyAsnGlnIyValAsnLeuLeuCyysArgSerMetArgLeuProH1sCyysSerLeuG 891
Db 2636 TGCCCGCCCGCCAGTGTACCTACTGTGTGACGCTCTGACGACAGGAGTGCAGCTGC 2695

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Qy 891 InArgLeuMetLeuAsnGlnCyH1sLeu 900
Db 2696 AGACCTCAGCTGCGCTGTGTGAGCTG 2724

RESULT 12
US-10-781-294-58
; Sequence 58, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PNAZ Domain-Containing Polypeptides,
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10/781,294
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)...(2332)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (306)...(458)
; OTHER INFORMATION: n = A,T,C or G
US-10-781-294-58

Alignment Scores:
Pred. No.: 2,19e-60 Length: 2524
Score: 705.00 Matches: 178
Percent Similarity: 47.91% Conservative: 131
Best Local Similarity: 27.60% Mismatches: 250
Query Match: 9.97% Indels: 86
DB: 3 Gaps: 12

US-10-066-521-6 (1-1344) x US-10-781-294-58 (1-2524)
Qy 50 IlegIAsnAlaAsnValGluCyLeuAlaLeuLeuH1sGluTyrrTyroIyAlaSer 69
Db 476 GTTTCGAATCCCACTGTATATGCGAGAGACAGCATTTGAAGAGAGTGGCTTTA 535
Qy 70 LeuAlaTrpAlaThrSerIleSerIlePheGlnMetAsnLeuArgThrIleuSerGlu 89
Db 536 CTGAGATCCTTTGAGAAATCTTATTGTGAAATGAAG-----AAAGATTACCTGAG 589
Qy 90 LysAlaArgAspAspMetIysIysIleSerGlnAlaMetGlnGlnGlnIyAlaThrAla 109
Db 590 AAGTACAGAAAGTACGTGAGAGAGACAGATTCCAGTGCATTGAAGACAGAAAGCCGTCTG 649
Qy 110 AlaGluThr-----GluGlnGlnGlu 116
Db 650 GGTGAGAGTGTGAGCTTCAAAACGCTTACACAGCACTGCCCTCATCAGAGGACCGG 709
Qy 117 IleserGlnAlaMetGlnGlnGlnIyAlaThrAlaAlaGluThrGlnGlnGlnIyH1s 136
Db 710 AGCAGCAGAGAGAGGAGACAGAGCTTGTGCGCATCGCAGAGAC----- 754
Qy 137 GlyIyAspThrTrpAspTyrlsSerH1sValMetThrLysPheAlaGluGluAsp 156
Db 754 ----- 754

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QY 443 AlValGluGluValTPrAsnArgLysSerValPheAspGluAspAspLeuMetValGln 462
 DB 112 GCTGACGAGGAGCTGTGTCGAGCACTTGAATTCAGTGGTGAAGACTGAGATGCTT 171
 QY 463 G1LeuGluGluSerGluLeuArgAlaLeuPheNhiIleLeuLeuProAspSer 482
 DB 172 GGGTTTACTAGGCTGATGCTGTGTGTGTGCGAGCGCGGAAATATCTTTTCCGAGCAAC 231
 QY 483 HisCysGluGluTyrTyrThrPhePheNhiIleuSerLeuGlnAspPheCysAlaIleu 502
 DB 232 ACTCATAAAGACCCCTTACAGTTCATACATTGAACCTCCAGGAGATTGTGTGACGCACT 291
 QY 503 TyrTyrValLeuGluGluLeuGluIleuProIleuValCysProLeu 518
 DB 292 GCATTTCTG-----ATGCAAGTACCCCACTATGATCCCTCCAGGACGACAGAG 342
 QY 519 TyrValGluTyrValArgSerMetGluLeuValGlnAlaGluPheNhiIleIleSer 538
 DB 343 TATTAAGAGAGAGAAACAATCTGACTTATCA----- 381
 QY 539 LeuTrpMetLysArgPheLeuPheGluLeuValSerGluAspValArgArgProLeuGlu 558
 DB 382 -----GTGTTACTTTCATTTGCGTCTCTAAATGCAACAGGAGAAATGCTTGAG 435
 QY 559 ValLeuLeuGluCysProValProLeuGluValLysGluLysLeuNhiIleTrpValSer 578
 DB 436 ACATCTTTTGATACCAAGTACCCAGTGTGAGACAGCTTCAAG-----TGAGACTCG 486
 QY 579 Leu-----LeuG1GlnGlnProAsnAlaThrThrProGluAspThrLeu 593
 DB 487 GTGGGATACATGAACAATTTGACACCTGACCCGAAAGATTGAGC-----CACATATG 540
 QY 594 AspAlaPheNhiIleuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsn 613
 DB 541 CCTTGTTTACTGCTCTATGAGATCGGAGAGAAATTTGTGAACAGATTTGTCGAT 600
 QY 614 SerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerPhe 633
 DB 601 GCTTCATGAGAGTTACAGTTTACCTTCATTCAGCAACAGATATGATGCTCATTAATC 660
 QY 634 CysLeuGlnNhiIleCysProTyrLeuArgLysIleArgValAspValLysGluIlePhePro 653
 DB 661 TGTCTGATTTACTGTCTGCTACCTGAGACACTTAAGTTGAGGTTCACGCGATCTTCAA 720
 QY 654 ArgAspGluSerAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeu 673
 DB 721 AACAAAGAG-----CCACTTATA----- 738
 QY 674 IleGluGluGlnTrpGluAspPheCysSerMetLeuGluThrNhiIleuArgGln 693
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 QY 694 LeuAspLeuGluSerSerIleuThrGluArgAlaMetLysThrLeuCysAlaLysLeu 713
 DB 738 ----- 738
 QY 714 ArgNhiIleuPheCysLeuIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlu 733
 DB 739 ---AGGCCAATCTGAGTGTGCTCATGTC-----TCGACTGCTTCTGCT 780
 QY 734 ValGlnNhiIleuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlu 753
 DB 781 TTGAAAGACTTACTACAGGCTTGTGCTGTAACTGAGAGCTG----- 822
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 DB 822 ----- 822
 QY 774 CysLeuLeuGluSerLeuArgLeuAspCysCysGluLeuThrNhiIleCysTyrLeuLys 793
 DB 823 -----ACATACCTGAGT 834

QY 794 IleSerGlnIleuThrThrSerProSerLeuLysSerLeuSerLeuAlaGluAsnLys 813
 DB 835 ATCAAC-----TGAGTCCATTTCCCTAAATATGTTTCACTT----- 873
 QY 814 ValThrAspGlnGluValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeu 833
 DB 874 -----CTGCATACACCTCTGCACGAGCCCAATGCCAATATA 909
 QY 834 GlnLysLeuIleLeuGluAspCysGluIleThrAlaThrGluCysGlnSerLeuAlaSer 853
 DB 910 AGTCATCTGAGCTTGAAATGATGATTTGCGACGCGCAAGATCGAAATGCGCTCT 969
 QY 854 AlaLeuValSerAsnArgSerLeuThrNhiIleuCysLeuSerAsnAsnSerLeuLysAsn 873
 DB 970 CTCTCATACAGTGGCGGAGCTGAGAAATGACCTTATTCAGCAATCCGCTGAGAGC 1029
 QY 874 GluGluValAsnLeuLeuCysArgSerMetArgLeuProNhiIleCysSerLeuGlnArgLeu 893
 DB 1030 GACCGAGTGAACATACGTGTGATGCTGCTGTCATGCCAATGCCAATCTTATATGACTG 1089
 QY 894 MetLeuAsnGlnCysNhiIleuAspThrAlaGluCysGluPheLeuAlaLeuMet 913
 DB 1090 GTGTAGTCTTCTGTCTGATTTGAATTCCTGACGCGCTTGGAAAGTCTTCTG 1149
 QY 914 GluAsnSerTrpLeuThrNhiIleuSerLeuSerMetAspProValGluAspAsnGluVal 933
 DB 1150 TTCAAGCCCACTGTAAAGCAATAGACTGTGTGATGATGCTTAAATAATTAAGAGATG 1209
 QY 934 LysLeuLeuCysGluValMetArgGluProSerCysNhiIleuGlnAspLeuGluVal 953
 DB 1210 TTGCATGTGAGGTTTCCCTGCTGCTGTTCCAACTGTCAAGTGTGAGAGACTTCATGCT 1269
 QY 954 LysCysNhiIleuThrAlaAlaCysGluSerLeuSerCysValIleSerArg 973
 DB 1270 GCGTGTCTTCTTACGAGGATATCTGTCAATATATGCCATAGTATTTACTCATATGA 1329
 QY 974 HisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGluLysArgGluValAlaAlaLeu 993
 DB 1330 AAATGAGAGACCTGTGAGATTTGGAGAGCAAAATAGAAATGAGAGATGACGTGCTA 1389
 QY 994 CysGluGluLysLysGluLysAsnSerValLeuThrArgLeuGluLysLysAlaCysGlu 1013
 DB 1390 TGTGCTGTGTGAGACATCCCACTGCAATGTTGTGATATATTTGGCTTGAAGAGTGCATG 1449
 QY 1014 LeuThrSerArgCysCysGluAlaLeuSerLeuAlaLeuSerCysAspArgNhiIleuThr 1033
 DB 1450 TTAAACAAGTGCCTGTGTGATCTTGTGCTGCTTGTACCAACCAACAACTTGA 1509
 QY 1034 SerLeuAsnLeuValGlnAsnAspPheSerProLysGluMetMetLysLeuCysSerAla 1053
 DB 1510 AGACTCAACTTGTCTTAATAATCACCTTGGCGCAATATGAGATTTGCAAACTTGTGAGAGC 1569
 QY 1054 PheAlaCysProThrSerAsnLeuGlnIleIleGluLeuTrpLysTrpGlnTyrProVal 1073
 DB 1570 TTGATCACCCAGATTTGTGACTTAAGGTAGTGGCTTCATTAATCAGGCTGAACACA 1629
 QY 1074 GlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlu 1093
 DB 1630 CAAAACCAAGCTGTCTATGATCTTAAGAAAGAAAGAAACCAAGTTATATCTTTGTGCT 1689
 QY 1094 SerTrpHisSerPheAspGluAspArgArgNhiIleGluLysLeuThr 1109
 DB 1690 GAAACTTGCTTTTAAAGAAAGC-----AGAGAAATTTGGTGTGACA 1731
 RESULT 14
 US-10-781-294-19
 ; Sequence 19, Application US/10781294
 ; Patent No. 6953691
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Godzik, Adam
 ; APPLICANT: Chu, Zhi-Liang
 ; APPLICANT: Pawlowski, Krzysztof

```

1  APPLICANT: Fiorentino, Loredeana
2  APPLICANT: Ariza, Maria Eugenia
3  APPLICANT: Stehlik, Christian
4  TITLE OF INVENTION: PAD Domain-Containing Polypeptides,
5  TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
6  FILE REFERENCE: P-1/1 4816
7  CURRENT APPLICATION NUMBER: US/10/781,294
8  CURRENT FILING DATE: 2004-02-17
9  PRIOR APPLICATION NUMBER: US/09/965,621
10 PRIOR FILING DATE: 2001-09-25
11 PRIOR APPLICATION NUMBER: US 09/671,760
12 PRIOR FILING DATE: 2000-09-26
13 NUMBER OF SEQ ID NOS: 64
14 SOFTWARE: FaSTSeq for Windows Version 4.0
15 SEQ ID NO 19
16 LENGTH: 2046
17 TYPE: DNA
18 ORGANISM: Homo sapien
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: (1) ... (2043)
22 US-10-781-294-19

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Db      1660 CACATGGAGCTTTCTTATTCGGTTTCTGAACAGAGCCGCTGGCCGCTGGAACAG 1719
Qy      560 LeuLeuGlyCysProValProLeuGlyValYlyLeuLeuHisTrpValSerLeu 579
Db      1720 TCATTCGAATGCAAGTGTCTTTCGGTAAAGAGAACTGCTGAAGTATCATCTCTG 1779
Qy      580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeu---AspAlaPheHisCys 598
Db      1780 TTG---CATTAATGATGACCACTTCTCCGACAGTGGGGTCCCGCACTTATCTACTGT 1836
Qy      599 LeuPheGlnThrGlnAspLeuGlyGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db      1837 CTCGATGAATATCCGGAGAGAACCTTTGTAAGCCAGCCCTAAATGATATCATTAAGTT 1896
Qy      619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
Db      1897 GCTTGAGAAATTTGGCAACAACAAAGAGATTCAAGTGTCTGCTTTTGGCTGAAAGCGTGT 1956
Qy      639 ProTrpLeuArgIleArgValAspVal 648
Db      1957 CAATATTTCATGAGTGAACCTGACCGTC 1986

RESULT 15
US-08-910-731-3
Sequence 3, Application US/08910731
Patent No. 5932440
GENERAL INFORMATION:
APPLICANT: CHATTERJEE, DEB K.
APPLICANT: SHANDILYA, HARINI
TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,731
FILING DATE: (Herewith)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1374 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

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LOCATION: 1..1368
US-08-910-731-3
Alignment Scores:
Pred. No.: 2,54e-53 Length: 1374
Score: 630.50 Matches: 151
Percent Similarity: 51.38% Conservative: 73
Best Local Similarity: 34.63% Mismatches: 205
Query Match: 8.91% Indels: 9
DB: Gaps: 3

US-10-066-521-6 (1-1344) x US-08-910-731-3 (1-1374)
Qy      653 ProArgAspGlnSerAlaGluAlaCysProValValProLeuTrpMetArg-----Asp 670
Db      39 CCGGAGCAAGAGCTCTCCCTGATATCCAAATATCAAG-TGGTC-AGGGTGATGAC 96
Qy      671 LysThrLeuIleGlnGlnGlnTrpGlnAspPheCysSerMetLeuGlyThrHisProHis 690
Db      97 TGTGGCTCATGAAAGTGGGTCGAGCAAGATCATGAGTCAGAGATCCAGGCCAACCTGCC 156
Qy      691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLeuThrLeuCys 710
Db      157 CTGACAGAGCTCAGGCTTACGCAACCAATGACTGGGTGATGCTGTGGTGGTGGTCTC 216
Qy      711 AlaLysLeuAsnHisProThrCysLeuYsIleGlnThrLeuMetPheArgAsnAlaGlnIle 730
Db      217 CAGGCTCTGCAAGATATCCATCTTGAAGTCCAGAAAGCTGAGCTTCAGAACTGCAAGCTTG 276
Qy      721 Thr---ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSer 749
Db      277 ACGGAAGCTGGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGA 336
Qy      750 LeuAsnLeuGlyGlyThrHisLeuLysGlnGlnAspValArgMetAlaCysGlnAlaLeu 769
Db      337 CTACATCTCAATGACCAACCTCTGGGGATGAGAGCTGGAAGCTGCTGTGAAGAGACTC 396
Qy      770 LysHisProLysCysLeuLeuGlnSerLeuArgLeuAspCysCysGlyLeuThrHisAla 789
Db      397 CGGACCCCGAGCTGCTGCTGGAAGAGCTTCAAGTGAATACTGTAACCTCAAGCTACC 456
Qy      790 CysTrpLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeu 809
Db      457 AGCTCGAGCCCTGGCTCAGTCCAGGAGCAAGCTTAAAGAGCTAGTAATTTG 516
Qy      810 AlaGlyAsnLysValThrAspGlnGlyValMetProLysSerAspAlaLeuArgValSer 829
Db      517 AGCAACAATGACTTCATGAGGCTGTATCCACACTGTGTGCAGGGCCCTGAAGATTC 576
Qy      830 GlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAlaThrGlyCysGln 849
Db      577 GCCTGTCAACTGGAATCTCAAACTGGAAGACTGTGATCACTACAGCCCACTGCAAG 636
Qy      850 SerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsn 869
Db      637 GATCTGTGTGATGTTGTGGCTCCAAAGGCTCAGCAAGGCTGGAAGTGGGCAAGC 696
Qy      870 SerLeuGlyAsnGlnGlyValAsnLeuLeuCysValArgSerMetArgLeuProHisCysSer 889
Db      697 AAGCTGGGCAACACAGGATTCAGACACTGTCTCAGGACTGTCTCCAGCTGCAG 756
Qy      890 LeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAla 909
Db      757 CTGAGGACTCTGTGGCTCTGGAGCTGTATGATGATGATGATGATGATGATGATGATGAT 816
Qy      910 LeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGlu 929
Db      817 CGTGCTCTAGAGCCAGAGAGCTGAAAGAACTCAAGCTAGGCTGAGCTAGAG 876
Qy      930 AspAsnGlyValLysLeuLeuLysCysGluValMetArgGlnProSerCysHisLeuGlnAsp 949
Db      877 GATGAGGGTGCACACTGCTGTGTGAGAGCTGTGAAGCTGTGGCTGTGAGCTGAGTGA 936

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